

RESULT 2
US-08-118-270-70
Sequence '70 Application US/08118270
Patent No. 5508384
GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
APPLICANT: Schubert, David I.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-70

Query Match 64.8%; Score 1571.5; DB 1; Length 345;
Best Local Similarity 90.8%; Pred. No. 4.1e-124;
Matches 324; Conservative 8; Mismatches 12; Indels 13; Gaps 7;

Db 301 AHSFAVRVLRGRTOKSIIHTSERGKVYTRPQARMIRLCKTLVILVVLLICRCPNL 360
Qy 361 AIMYDVFCKMKNLKTKTFAFCMSLCLLNSTNPILYALRSKDLRHAFRSMPPSC 420
Db 361 AIMYDVFCKMKNLKTKTFAFCMSLCLLNSTNPILYALRSKDLRHAFRSMPPSC 420
Qy 421 PLDNMGDSDCLKHANNAASVRAEAECKSTVKIAKVTMSVSTDTSAAEL 472
Db 421 PLDNMGDSDCLKHANNAASVRAEAECKSTVKIAKVTMSVSTDTSAAEL 472

Qy Qy 296 YILWKAHSHAVRMIQRGQTQKSIIHTSEDGKVQVTRPQARMIRLAKTLVILVVLLIC 355
Db Db 180 YILWKAHSHAVR-AQRSTQKSIIHTSEDGKVQVTRPQARMIRLAKTLVILVVLLIC 238
Qy 356 WGPLLAIMYDVFGRKNLKTTVAFPSMCLLNSTNPILYALRSKDLRHAFRSMPPSC 415
Db 239 WGPLLAIMYDVFG--LLIKTVEAFCSL-LINSTNPILYALRSKDLRHAFRS-WPSC 292
Qy Qy 416 EGTAQPLDNMGDSDCLKHANNAASVRAEAECKSTVKIAKVTMSVSTDTSAAEL 472
Db Db 293 EGTAQPLDNMGDSDCLKHANNAASVRAEAECKSTVKIAKVTMSVSTDTSAAEL 472
Qy Qy 296 YILWKAHSHAVRMIQRGQTQKSIIHTSEDGKVQVTRPQARMIRLAKTLVILVVLLIC 355

RESULT 3
PCT-US33-08528-70
Sequence 70 Application PC/TUS9308528
GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 70:
SEQUENCE CHARACTERISTICS:
LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US33-08528-70

Query Match 64.8%; Score 1571.5; DB 4; Length 345;
Best Local Similarity 90.8%; Pred. No. 4.1e-124;
Matches 324; Conservative 8; Mismatches 12; Indels 13; Gaps 7;

Db 1 LAIAVLSLT-LGTFIVLENLLVLCVILSRSLCRPSHFIGSLAVADLLGSVFTYYSPI 175
Qy 117 LAIAVLSLT-LGTFIVLENLLVLCVILSRSLCRPSHFIGSLAVADLLGSVFTYYSPI 175
Db 1 LAIAVLSLT-LGTFIVLENLLVLCVILSRSLCRPSHFIGSLAVADLLGSVFTYYSPI 60
Qy 176 DFHVFRKDSRNVLFLKGCGTASFTASVGSFLTARYISIHRPLAYKRVTRPKAVV 235
Db 61 DFHVFRKDSRNVLFLKGCGTASFTASVGSFLTARYISIHRPLAYKRVTRPKAVV 120
Qy 236 AFCLMWTIAVIAVPLLGWNLKQSCDIPPHIDETYLMPWIGHTSVLLFIVYAYM 295
Db 121 AFCLM-TIAVIAVPLGWNCCKLQSYCCDIPPLDGTYLMPWIGHTSVLLFIVYAYM 179
Qy 296 YILWKAHSHAVRMIQRGQTQKSIIHTSEDGKVQVTRPQARMIRLAKTLVILVVLLIC 355

RESULT 4
 US-09-826-509-471
 Sequence 471, Application US/09826509
 Patent No. 6806054
 GENERAL INFORMATION:
 APPLICANT: Lehmann-Bruinsma, Karin
 APPLICANT: Lin, I-Lin
 TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G Protein-Coupled Receptors
 FILE REFERENCE: AREN-207
 CURRENT APPLICATION NUMBER: US/09/826,509
 PRIORITY NUMBER: 2001-04-05
 PRIORITY FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: 60/195,747
 PRIORITY FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 589
 SOFTWARE: Patentin Version 2.1
 SEQ ID NO: 471
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-826-509-471

Query Match 29 1%; Score 705; DB 2; Length 360;
 Best Local Similarity 44.8%; Pred. No. 2.e-51; Gaps 6;
 Matches 148; Conservative 57; Mismatches 95; Indels 30; Gaps 6;

Qy 78 ITEPNKSLSSPKENENIQCQGENFDIECPMLNPSQQLAIAYLSLTLGTFTYLENLY 137
 Db 6 VTEIANGSKDGSNS-----PMQDMYLSPQKTAVALCTLGSALENAV 54

Qy 138 LCVLHRSRSCRPSTYFIGSLAVADLGSVTFYSPIDPRVERKDSRNVLFLKGVT 197
 Db 55 LYLISSHQLRKPSYTFIGSLAGDFLASVFAESPVNTHFEGYDSSKAVELLKIGSVT 114

Qy 198 ASFTASVGSLPLTATARYISIHRPLAYKRVTRPKAVAPCLMNTIAIVAPLLGWN 257
 Db 115 MIFTASVGSLLTADRLCIRYPKXALITGRALVTLGIMWVLSALSYPLMGWC 174

Qy 258 EKLOSVQSDIPPHIDETYLMPWIGTSVLLFLIVYAYMYILWKASHAVMIGRGTQKSI 317
 Db 175 --CPRPSELPELPIPDYLSWLLFTAFLFSGLITYGHYLMKAHOVA-----SL 223

Qy 318 IHTSEGKVOTRPGARMA--IRLAKTVLILVWVLIICGPLAIVMDVFGMKLII 375
 Db 224 SGH--QRQV---PGMARWLDVRKLTKLGVIVLICMFPVLMAMSLATTLSQV 277

Qy 376 KTVFAFGSMLCLINSTNPYIYALRSSDLR 405
 Db 278 KKAFAFGSMLCLINSMNPYIYALRSSBR 307

RESULT 5
 PCT-US96-10618-3
 Sequence 3, Application PC/US9610618
 GENERAL INFORMATION:
 APPLICANT: Coileman, Roger
 APPLICANT: Guebler, Karl J.
 APPLICANT: Au-Young, Janice

RESULT 6
US-09-169-205D-20
Sequence 20, Application US/09169205D
GENERAL INFORMATION:
APPLICANT: Erickson, James
APPLICANT: Goddard, J. Graham
APPLICANT: Kiefer, Michael
TITLE OF INVENTION: METHODS FOR DETECTING COMPOUNDS WHICH MODULATE THE FILE REFERENCE: 252/004
TITLE OF INVENTION: ACTIVITY OF AN LPA RECEPTOR
CURRENT FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 20
LENGTH: 364
TYPE: PRT
ORGANISM: Homo sapiens
US-09-169-205D-20

Query Match 15.0%; Score 364; DB 2; Length 364;
Best Local Similarity 27.9%; Pred. No. 1. 5e-22;
Matches 110; Conservative 70; Mismatches 44; Gaps 11;
Query 59 QERMTAGDNPOLVADQVNITEFYNSKSLSSFKENEEENIQCGENFMDECFMVLTNPSQLA 118
Db 13 QPQTAMNEPQC----FYNESAFFYNRSGRHLATE----WNTVSKLV 52
Query 119 IAVLSLTIGTFTVLENLVLVCILHSRSLRCPSPHFIGSLAVADLGSVITYVSFDHF 178
Db 53 MG-LGITYCIFIMANLIVMAYIAVNNRFHF-PITYVLMNLAADFFPAGLAYFYLMENTG 110
Query 179 VFHFKDSRNVFPLKGTVASFTASVGSLFTALARVTSIHRPLAYKRIVTRPKAVVAFC 238
Db 111 PNTRRLTVSTWLRLQGLDTSLAVANLLAERHTVFRMLHTRMSNE-RVVVVV 169
Query 239 LMNTIAVIALPLGLNCBKLQSQVCSDFIPHIDETYLMPNIGTSTVLLFLIVYAMYIL 298
Db 170 VITWMAITMGAIAPSGLNCICDIECNNSMAPLYSDSIVLFAINLYTFVWNVVLYAHF 229
Query 299 WKAHSHAVRMIOGTQKSIIIIHSEDGKVQTRPDQARMAFRAKTYLVLVLLIICWP 358
Db 230 GYVRQRTMRMSR----HSGPQRNRDT----MMSLKTIVVILGAFTTCWTP 273
Query 359 LIAIMYDVFGRMNKLIKTVFAFCSMICLNSTNPVIIYALRSKDLRHAFRSMFPSCEGT 418
Db 274 GLVLLLPVCCPOCDVL-AYEKFPLLAETFSAMPNPIYSTDKEMSATFRQL---C 327
Query 419 AQLDNSMGDSDCLHKHANN----AAVHRAAESCI 450
Db 328 CORSENPTGPTESSDRSASSLNLTLAGVHNSNDHSVV 364
RESULT 8
US-09-811-838-2
Sequence 2, Application US/09811838
GENERAL INFORMATION:
APPLICANT: Miller, Duane D.
APPLICANT: Tigray, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Sardar, Vineet M.
APPLICANT: Elrod, Don B.
APPLICANT: Xu, Huiping
APPLICANT: Baker, Daniel L.
APPLICANT: Wang, Dean
APPLICANT: Liliom, Karoly
APPLICANT: Fischer, David J.
APPLICANT: Virág, Tamás
APPLICANT: Nusser, No. 6875757a
TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
FILE REFERENCE: 20609/181
CURRENT APPLICATION NUMBER: US/09/811,838
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/190,370
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 364
TYPE: PRT

RESULT 7
US-09-731-030A-15
Sequence 15, Application US/09731030A
GENERAL INFORMATION:
APPLICANT: MUNROE, Donald G.
APPLICANT: GUPTA, Ashwani K.
APPLICANT: ZASTAWNY, Roman L.
TITLE OF INVENTION: MAMMALIAN EDG-7 RECEPTOR HOMOLOGS
CURRENT APPLICATION NUMBER: US/09/731, 030A
CURRENT FILING DATE: 1998-12-29
PRIOR APPLICATION NUMBER: 60/070,184

ORGANISM: Homo sapiens
US-09-811-838-2

Query Match 15.0%; Score 363; DB 2; Length 364;
Best Local Similarity 27.2%; Pred. No. 1-5e-22;
Matches 108; Conservative 72; Mismatches 167; Indels 50; Gaps 10;

Qy 59 QEKMTAGDNPQLPDAQVNITEFYKNSLSSPKENENIQGENFMIDICFMVNLNPSSQQLA 118
Db 13 QPQFTAMNEQC-----FINESIAFPYNSRGKHIAE-----WNTVSKLV 52

Qy 119 IAVLSLTIGFTPEULENLIVLCVILHSLRSLCRPSYTHIGSLAVADLGLSUVIYFSFIDFH 178
Db 53 MG-LGIVTCPIMLANLYMVAIYNRPRHF-PIYLMANLAADFPIAGLAYFYLMPRTG 110

Qy 179 VEHRIKDSRNVELFKUGGTASFTASVGSPLTLTARYISIHRPLAYKRIVTRPKAVVAF C 238
Db 111 PNTRLBLTVSTMLRQLDTSLTAVANLLAIAERHTVFRMQLHTMSNR-RVYVVIV 169

Qy 239 LMWTIAIVIAVLPLGWNCEKLOSVCSDFPHIDETYLFWFGTVSLLFLIVYAYMIL 298
Db 170 VIWTAIVMGAIPSYGNWCIDIECNCSNAPLYSSSYLWFAIINLVTFVWVVVLYAHIF 229

Qy 299 WKAHSHAVRMQIORTQKSIILHTSEDGVQVTRPQDARMAIRLAKTLVLLVVLJICRG P 358
Db 230 GYVRQRTMRNSR-----HSSCPRNRDT-----MMSLIKTVTIVLGAFICPTP 273

Qy 359 LLAIMVYDVFERMNKLKTVTAPFCNSMLCLLNSTVNPITYALRSKDLRAFRSMFPSCEGT 418
Db 274 GLVLLLDVCCPQCDVLY-AVEKFPLLAETNSAMPITISYRDKEMSATPRQIL----C 327

Qy 419 AQPLONSMGDSDCLHKHANN-----ASVHRAAESCI 450
Db 328 CORSENPTGPTESSDRASSLNHTTLAGVHSNDHSVV 364

RESULT 9
PCT-US96-10618-2

Sequence 2, Application PC/TUS9610618

GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
ADDRESSEES: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0042 PCT

FILING DATE: 12-DEC-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: JAHNS, Kristina M.
 REGISTRATION NUMBER: 41,092
 REFERENCE/DOCKET NUMBER: P8074-6018
 TELEPHONE: (202) 638-5000
 TELEXFAX: (202) 638-4810
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 364 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide

US-08-763-938-2

Query Match 14.6%; Score 355; DB 2; Length 364;
 Best Local Similarity 28.0%; Pred. No. 6.e-22;
 Matches 104; Conservative 68; Mismatches 166; Indels 34; Gaps 10;

Qy 81 FYNKSLSSFKNEENIQGENFMDIECFMVNLNPSQLIAVSLTLLGFTVLENLVLTCV 140
 Db 25 PYNEISAFFYRNRSKYLATE-----WNTVSKLMG-LGITVCVFIMANLVMVA 73

Qy 141 TIIHRSRSLCRPSYFIGSLAVADILGSYIIFTYSFIDFFIVFHFRKDSRANFLFLKGGMATASF 200
 Db 74 IYNNRRHF-PITYLMTAADEFGAGLAYFYMENENTPNTRELTVSMLLRQGLIDTSL 132

Qy 201 TASVGLSLTATAKYIISIRPLAYKRIVTRPKAVVAPCLMWTIAIVAVPLGMNCERKL 260
 Db 133 TASYNLALIAIERHTIVYFMRQLHTRMSNR-RVYVVIIVTMAVNGAIPSYGNNTCD 191

Qy 261 QSVCSDDPHIDENTMFWIGTSVSLIFIVAYAMYIIMLKASHAVRMHQRTQKSIIH 320
 Db 192 IDHCSNMNAPLYSDSYLVTFWAIFLNLTFTVMMVLYAHIFGYVRORTMSR-----H 242

Qy 321 TSEDGKVQVTRPDQARMARLAKTLYLILVLLCIGPILLAMVYDVGKMKNLIKTVFA 380
 Db 243 SSGRRRNRT-----WMSLLKTTVVIYLGAFITWCWTLGVLVLLDVCPCQCDVL-AYEK 294

Qy 381 FCSMLCLLNSTNPILYIYALRSKDLRHAWSRSMPPSCGEAQPLDNMSGDCLHKHANNA- 439
 Db 295 FELLAENSAMNPITYSTRDKEMSATPRQIL-CCQRHENPNPTEG-SDRSASSLNTTI 352

Qy 440 -ASVYRAASCI 450
 Db 353 LAGVHSNDHSVV 364

RESULT 11
 US-08-845-566-3 Sequence 3, Application US/088455566
 Patent No. 591244 GENERAL INFORMATION:
 APPLICANT: Au-Young, Janice
 APPLICANT: Guegler, Karl
 TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/845,566
 FILING DATE: Filed Herewith
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0271 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 181948

US-08-845-566-3

Query Match 14.6%; Score 353; DB 1; Length 381;
 Best Local Similarity 27.3%; Pred. No. 1.1e-21;
 Matches 102; Conservative 71; Mismatches 129; Indels 72; Gaps 12;

Qy 68 PQLVP-----ADQYI--ITEFYN----KSLSSFKNEENIQGENFMDIECFMVNL 111
 Db 3 PRSPVPLYKAHRSSVSDVNYDIVRHYTYTGKLINISADKENSIKL-----47

Qy 112 NPSQQLIAVLSKLTGTPTVLENLVLCVLHSRSLCRPSYHFGSLAVADILGSYIVF 171
 Db 48 -----TSVWTFILICCFILLENTFLTINTKTKPH-RPMYYFIGNLSDLAGVAYT 99

Qy 172 YSFIDDFVFRKDSRANVFLKGFTASFTASVGSFLTARYS-----IHRPLAYKR 226
 Db 100 ANILLSGATTYKLTPAONFLRGSMFTVALSASVFSLLAIALERYITMVKLHNGSNFR 159

Qy 227 IVTRPKAVVAFCLMMTIAIVAVPLPGLGNCKEKOSVCSDFPHIDETYLFWIGTVSVL 286
 Db 160 LP-----LILISAC--WVSLILGSLPTMGWNCI SALSSCSTVLPYHGHVILFCCTVFTLL 213

Qy 287 LIPIV--YAYMNTLWKASHAVRMHQRTQKSIIHINTSEDGKVQTRPDQARMARLAKT 344
 Db 214 LLSIVTLYCRIYSLVRETRSRLTF-----RKNISKASRSSENVALKT 256

Qy 345 LVNLWVLLICNGPLAIMVYDVGKMKNLIKTVF--AFCSMLCLLNSTNPILYALRSK 402
 Db 257 VIVLVSPIACTAPLFLILDVGCKV-KTCDILFRAEYFLVAVLNSGTNPITYLTNK 315

Qy 403 DLRAHAFRSMFPESC 416
 Db 316 EMRAFRIMSCCK 329

RESULT 12
 US-08-467-948A-28 Sequence 28, Application US/08467948A
 Patent No. 5998164 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polymucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR2
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 OPERATING SYSTEM: PC-DOS/MS-DOS
 COMPUTER: IBM PC COMPATIBLE
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,948A
 FILING DATE: 06-JUN-1995
 CLASIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 STRANDBEDNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-467-948A-28

Query Match 14.6%; Score 353; DB 1; Length 381;
 Best Local Similarity 27.3%; Pred. No. 1.1e-21;
 Matches 102; Conservative 71; Mismatches 129; Gaps 12;
 SEQ ID NO 18

TYPE: PRT
 ORGANISM: genomic
 US-08-852-824-18

Query Match 14.6%; Score 353; DB 2; Length 381;
 Best Local Similarity 27.3%; Pred. No. 1.1e-21;
 Matches 102; Conservative 71; Mismatches 129; Gaps 12;

68 PQLVPIVFCITLQVNLVCLGFTVLENLVLQVLSLRCRPSYHIGSLAVDILGSVIFV 171
 3 PTSVPLVKHRSSVSDYVNIDIVHNTYGRKLNSADENSIKL----- 47

68 PQLVPIVFCITLQVNLVCLGFTVLENLVLQVLSLRCRPSYHIGSLAVDILGSVIFV 171
 3 PTSVPLVKHRSSVSDYVNIDIVHNTYGRKLNSADENSIKL----- 47

112 NPQQQLAAVLSLTLGFTVLENLVLQVLSLRCRPSYHIGSLAVDILGSVIFV 171
 112 NPQQQLAAVLSLTLGFTVLENLVLQVLSLRCRPSYHIGSLAVDILGSVIFV 171
 48 -----TSVVFUJICCPITILENIVFLVLTWKTCKFH-RPMYYFGNQLSLLAGVAYT 99

Db 172 YSFIDFHVPHRKDSBRNVFLPKLGTVTASTASVSLFTAIARYIS----IPLAYERKR 226
 Db 100 ANLLSGATTYKLTPAQWFLREGSMFEVALSASVSSLLAIAERYITMLKMKLNGSNNFR 159
 Db 227 IVTRPKAVVAFCLMNTIAVIAVFLPGLGNCCEKIQSVCSDFPHIDETYLFWIGVTSVL 286
 Db 160 LP----LLISAC--WVISLUGGLPIMGNICISALSSCSTVLPYHKGHLFCFTVFTLL 213
 Db 287 LLPTV--YAMYLWKAHSHAVRMQIQTOKSIIIIHTSBDGVQVTRPDOARMAIRLAKT 344
 Db 214 LLSIVVLYCRISSLVTRRSRLTF-----RNKISKAARSSENVALKT 256
 Db 345 LVLIVLVLICWGPILLAIMYDVGRMNKLTKTF--AFCSMLCLNSTNPYIALRSK 402
 Db 257 VIVLSVPIACWAPLFLILLDGCKV-KTCDCILFRAEYFLVLAIVNSGTNPITYLTNK 315
 Db 403 DLRAFAFRSMFPSC 416
 Db 316 EMRAFIRIMSCCK 329

RESULT 14
 US-08-467-947A-28
 Sequence 28, Application US/08467947A
 Patent No. 6090575
 GENERAL INFORMATION:
 APPLICANT: LI, YI
 APPLICANT: CHAO, LIANG
 APPLICANT: NI, JIAN
 APPLICANT: GENTY, REINER
 APPLICANT: BULT, CAROL J.
 APPLICANT: SUTTON III, GRANGER G.
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
 TITLE OF INVENTION: Coupled Receptor GPR1
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVE., NW, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PAVENTIN RELEASE #1.0, VERSION #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/467,947A

RESULT 13
 US-08-852-824-18
 Sequence 18, Application US/08852824C
 Patent No. 6050272
 GENERAL INFORMATION:
 APPLICANT: Li et al.
 TITLE OF INVENTION: Human G-Protein Coupled Receptors

FILING DATE: 06-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA: PCT/US95/04079
 FILING DATE: 30-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: STEEPE, ERIC K.
 REGISTRATION NUMBER: 36 688
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEX/FAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 381 amino acids
 TYPE: amino acid
 STRANDBNESS: single
 TOPOLOGY: not relevant
 MOLECULE TYPE: peptide
 US-08-467-947-A-28

Query Match 14.6%; Score 353; DB 2; Length 381;
 Best Local Similarity 27.3%; Pred. No. 1.e-21;
 Matches 102; Conservative 71; Mismatches 129; Indels 72; Gaps 12;

Query 68 PQLVPP-----ADQVN---ITEFYN---KSLSSFKENENIQGGENFMDIECFMVL 111
 3 PTSVPLVKAHRSVSDYNYDIVERHTNTGKLNIISAKENSKL----- 47

Query 112 NPSQQLAIAVLSLTGLGFTVLENLVLVCLHSRLCRPSYHFIGSAAVADLGSYTFV 171
 48 -----TSVVVFLLICCPFILENFWLTIWTKKFH-RPMYFIGNLASDLAGYAT 99

Query 172 YSFIDFHVFRKDSRANVFLKGVTASFTAVSGSLFLTARYIS---IHRPLAYKR 226
 100 ANILSGATTYKLTPTAOFLREGSMFVALSASVSLIAIERYITMLKMLHNGSNFR 159

Query 227 IVTRPKAVVAFCLMWTAIVIAVPLLGNCBKLQSVDIIPHIIDETYLMPWIGTVSL 286
 160 LF---LLISAC---WVSLILGGPIMGNCISALSSCSTVPLYHGHYILFCTVTLLT 213

Query 287 LAPIV--YAYMILWKAHSHAVRMIORGQTQSIIHTSEDGKVQVTRPDQAMAIRLAKT 344
 214 LLSIVILVCRYSLVRTSPRSRLTF-----RKNIKASRSSSENVALLKT 256

Query 345 LVLLVLLICMGPILLAMIVYDVGKMKLIKTVF--AFCSMCLINSTVNPIIYALRSK 402
 257 VIVLVSPIACWAPLFLILLDGGCKV-KTCDFLFRAYFLVAVLNSTGNPIIYTLLNK 315

Query 403 DLRAFAFSMFPSC 416
 316 EMRAFTRIMSCCK 329

Search completed: January 6, 2006, 21:13:17
 Job time : 48 sec(s)

RESULT 715
 US-09-731-030A-17
 Sequence 17, Application US/09731030A
 Patent No. 6566996
 GENERAL INFORMATION:
 APPLICANT: MUNROE, Donald G.
 APPLICANT: GUPTA, Ashwani K.
 APPLICANT: ZASTAWNY, Roman L.
 FILE REFERENCE: 8074-0015
 CURRENT APPLICATION NUMBER: US/09/731, 030A
 PRIOR APPLICATION NUMBER: 1998-12-29
 PRIOR FILING DATE: 1997-07-01
 NUMBER OF SEQ ID Nos: 21
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 17
 LENGTH: 381
 TYPE: PRT

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OM protein - protein search, using sw mode1

Run on: January 6, 2006, 21:00:32 ; Search time 189 Seconds

Title: US-10-521-420-1
Perfect score: 2424
Sequence: 1 MKSILDGLADTFRTTITDLS.....TVKIAKVTMSVSTDTSAAEL 472
1097.285 Million cell updates/sec

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_21:*

1: geneseqp1390b: *
2: geneseqp1390b: *
3: geneseqp2000b: *
4: geneseqp2001b: *
5: geneseqp2002b: *
6: geneseqp2003ab: *
7: geneseqp2003bs: *
8: geneseqp2004b: *
9: geneseqp2005b: *

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Adh77048

1: Adh77048 hcB-1 D21
Aar14196 Human can
Abp5825 Human can
Abp81800 Human Pro
Add46383 Human Pro
Adl15025 Human CB1
Adn38918 Cancer/an
Abo60051 Human Gen
Ado29561 Human GPC
Aea81221 Human can
Aeb56338 Non-endog
Adn38920 Cancer/an
Aar14195 Rat canna
Add46381 Rat Prote
Abp57048 Mouse isc
Ado29562 Mouse GPC
Adm82794 Human can
Adu82881 Ligand up
Adj70504 Human hea
Adn38922 Cancer/an
Aea81222 Human can
Aar48749 G-protein
Aaw02721 G-protein
Adq97953 Mouse can

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2424	100.0	472 8 ADH77048	Adh77048 hcB-1 D21 Aar14196 Human can
2	2412	99.5	472 2 AAR14196	Abp5825 Human can
3	2412	99.5	472 6 ABR5825	Abp81800 Human Pro
4	2412	99.5	472 6 ABR5825	Add46383 Human Pro
5	2412	99.5	472 7 ADD46383	Adl15025 Human CB1
6	2412	99.5	472 7 ADL15025	Adn38918 Cancer/an
7	2412	99.5	472 8 ABO60051	Abo60051 Human Gen
8	2412	99.5	472 8 ADO29561	Ado29561 Human GPC
9	2412	99.5	472 9 AEAB81221	Aea81221 Human can
10	2412	99.5	472 9 AEAB81221	Aeb56338 Non-endog
11	2409.5	91.2	472 4 ABP56338	Adn38920 Cancer/an
12	2401	99.1	472 7 ADN38920	Aar14195 Rat canna
13	2333.5	96.7	473 2 AAR14195	Add46381 Rat Prote
14	2343.5	96.7	473 7 ADD46381	Abp57048 Mouse isc
15	2340.5	96.6	473 5 ABP57048	Ado29562 Mouse GPC
16	2340.5	96.6	473 8 ADO29562	Adm82794 Human can
17	2209.5	91.2	439 8 ADM82794	Adu82881 Ligand up
18	2133.5	88.0	789 8 ADU82881	Adj70504 Human hea
19	1954	80.6	411 7 ADJ70504	Adn38922 Cancer/an
20	1954	80.6	411 7 ADN38922	Aea81222 Human can
21	1954	80.6	411 9 AEAB81222	Aar48749 G-protein
22	1971.5	64.8	345 2 AAW02721	Aaw02721 G-protein
23	1571.5	64.8	345 2 ADQ97953	Adq97953 Mouse can
24	735.5	30.3	363 8 ADQ97953	

ALIGNMENTS

RESULT 1

ID ADH77048 standard; protein; 472 AA.
XX
AC ADH77048;
XX
DT 22-APR-2004 (first entry)

XX hCB-1 D213A double mutant, SEQ ID 1.

XX DB 22-APR-2004

XX XX

XX hCB-1 D213A double mutant, SEQ ID 1.

XX DB

XX XX

XX Anorectic; neuroprotective; cardiovascular; respiratory;

XX gastrointestinal; cannabinoid; CB; receptor; obesity; psychiatric;

XX neurological; immune; cardiovascular; reproductive; endocrine; disorder;

XX respiratory; gastrointestinal; hCB-1 D213A; mutein.

XX Homo sapiens.

OS Synthetic.

XX OS

XX PN WO2004008150-A1.

XX XX

XX WO2004008150-A1.

XX XX

XX PD 22-JAN-2004.

XX XX

XX PF 14-JUL-2003; 2003WO-GB003066.

XX PR 17-JUL-2002; 2002SE-00002242.

XX PA (ASTR) ASTRAZENECA AB.

XX PA (ASTR) ASTRAZENECA UK LTD.

XX PI Greasley P,

XX PI WPI; 2004-143121/14.

XX PR

XX PT 14-JUL-2003; 2003WO-GB003066.

XX PT Identifying an inverse agonist of a cannabinoid (CB) receptor, useful in

CC The invention relates to a method for identifying an inverse agonist of a

CC cannabinoid (CB) receptor comprising contacting a CB receptor test

CC inhibitory agent with the cell expressing the constitutively active CB

CC receptor. The method is useful in preparing a disorder associated with a CB

CC receptor. The true antagonist or inverse agonist is useful in preparing a

CC medicament for treating or preventing a disorder associated with a CB

CC receptor. The disorder is obesity, psychiatric and neurological

CC disorders. They are also useful in treating immune cardiovascular, CC reproductive and endocrine disorders and also diseases related to CC respiratory and gastrointestinal systems. The current sequence represents CC the amino acid sequence of the hCB-1 D213A double mutant.

XX Sequence 472 AA;

Query Match 100.0%; Score 2424; DB 8; Length 472;
Best Local Similarity 100.0%; Pred. No. 2.2e-241; Indels 0; Gaps 0;
Matches 472; Conservative 0; Mismatches 0; Gaps 0;

QY 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

DB 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

QY 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

DB 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

QY 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

DB 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

QY 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

DB 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

QY 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

DB 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

QY 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

DB 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

QY 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

DB 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

QY 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

DB 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

RESULT 2
AARI14196 standard; protein; 472 AA.

XX AARI14196;

XX 25-MAR-2003 (revised)

DT 17-DEC-2001 (revised)

DT 19-DEC-1991 (first entry)

DB Human cannabinoid receptor.

XX Cannabis sativa; marijuana; drug test; substance K receptor.

XX Homo sapiens.

PN USN7564075-N.

XX 03-SEP-1991.

XX 08-AUG-1990; 90US-00564075.

XX 08-AUG-1990; 90US-00564075.

XX (USDC) NAT INST OF HEALTH.

PA (USDC) US SEC OF COMMERCE.

XX Matsuda L, Brownstein M;

XX

DR WPI; 1991-303326/41.
DR N-PSDB; AAQ14003.

XX DNA encoding mammalian cannabinoid receptor - used for producing receptor
XX for screening drugs and ligands and in detection.

XX Disclosure; Fig 5; 25pp; English.
XX

CC SKR6 cDNA encoding the rat cannabinoid receptor was isolated from a rat
CC cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a
CC human cosmid library. A positive clone was identified and sequenced.

CC There is ca. 97 per cent homology between this amino acid sequence
CC deduced from the sequence of the positive human clone and rat cannabinoid
CC receptor (see AR14195). Recombinantly produced receptor can be used to
CC screen for new drugs suitable for treatment of cannabinoid-treatable
CC conditions, e.g. glaucoma, bronchial asthma, etc. (Note: Revised entry
CC submitted to correct the patent number format of US Government-owned NTRIs
CC applications to prevent clashes with ongoing US granted patent numbers.
CC For further information please visit the Derwent web site at
CC www.derwent.com/dwp1/updates/ntris_us.htm.) (Updated on 25-MAR-2003 to
CC correct PA field.)

XX Sequence 472 AA;
SQ Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 2;
Best Local Similarity 99.6%; Pred. No. 3.8e-240; Indels 0; Gaps 0;

Matches 470; Conservative 0; Mismatches 0; Gaps 0;
Matches 470; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

DB 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

QY 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

DB 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

QY 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

DB 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

QY 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

DB 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

QY 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

DB 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

QY 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

DB 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

QY 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

DB 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

QY 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

DB 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

QY 472 AA;

DB 472 AA;

QY 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

DB 1 MKSLIDGLADDTPTITTDLYLQGSNDIQEDIKGDMASKLGYPQKPLTSFRGSPPQE 60

QY 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

DB 61 KMTAGDNPLVPAQVNTEFYNSKLSSPKENENIQGENFMIDIECMVNLAPSQQLIA 120

QY 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

DB 121 VLSLTLGFTVLENLLVLCVILHRSRSLCRPSYTHFIGSLAVADLLGSYIYFSFIDPHVF 180

QY 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

DB 181 HRKDSRNVFLFKLGTVTAFTASVGSLETTAIARYISTHRPLAYKRTVTRPKAVAFCLM 240

QY 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

DB 241 WTAIVAVIAVPLIGWNCEKLSQVCSIDIPHIDETYLWIGTYSVLLPIVAYAMYTLWK 300

QY 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

DB 301 AHSHAVRMQIORTGOKSIIHTHSEDGKVOTRPOARMAIRLAKTLVLLVLLJICMGPLL 360

QY 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

DB 361 AIMYYDVGKMKNLIKTYFAFCSMCLCNSTNPITYALRSIDLHAFRSMPSCECTAQ 420

QY 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

DB 421 PLDNMGSDCLHKHANNAASVRAAESCIKSTVKIAYVMTSYSTDTSAAEL 472

RESULT 3

ID ABR5855

ID ABR58525 standard; protein; 472 AA.

XX ABR58525;

XX DT 09-JUL-2003 (first entry)

XX Human cannabinoid receptor 1 (brain) protein.

XX DE

XX KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;

XX heart disease; atherosclerosis; endometriosis.

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g., AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension, or
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABP1623 to ABP2869 encode
 CC GPCR proteins given in ABP1675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX

Sequence 472 AA;

Query Match 99.5%; Score 2412; DB 6; Length 472;

Best Local Similarity 99.6%; Pred. No. 3.8e-24; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy      1 MKSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60
Db      1 MKSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60
* Qy      61 KMTAGDNPOLYPDAQVNTEFYKNSLSSFKENENIQGENFMIDECMVNLNPSSQIA 120
Db      61 KMTAGDNPOLYPDAQVNTEFYKNSLSSFKENENIQGENFMIDECMVNLNPSSQIA 120
Qy      121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180
Db      121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180
Qy      181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240
Db      181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240
Qy      241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300
Db      241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300
Qy      301 AHSHAVRATORGTOKSIIHTSEDGKVQTRPQARMIRAKLTIVLIVVLIICMGPILL 360
Db      301 AHSHAVRATORGTOKSIIHTSEDGKVQTRPQARMIRAKLTIVLIVVLIICMGPILL 360
Qy      361 AIMYYDVFGRMNKLKITVAFCSMLCLNSTVAPIYALRSKDRLHAFRSMPSCBGTAAQ 420
Db      361 AIMYYDVFGRMNKLKITVAFCSMLCLNSTVAPIYALRSKDRLHAFRSMPSCBGTAAQ 420
Qy      421 PLDNSMGSDCLKHANNAASVRAEESCIKSTVKIAKVTMSVSTDISAEAL 472
Db      421 PLDNSMGSDCLKHANNAASVRAEESCIKSTVKIAKVTMSVSTDISAEAL 472

```

RESULT 5

ADD46383 ADD46383 standard; protein; 472 AA.

XX ADD46383;

XX 29-JAN-2004 (first entry)

XX Human Protein P21554, SEQ ID NO 12063.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; SNI; Chung.

KW Homo sapiens.

PN WO2003016475-A2.

XX

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PD 27-FEB-2003.
XX 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P21554.
XX PR New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX Claim 1; Page: 1017PP; English.
XX PS Claim 1; Page: 1017PP;

```

The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The compound or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC the sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

Sequence 472 AA;

```

Query Match 99.5%; Score 2412; DB 7; Length 472;
Best Local Similarity 99.6%; Pred. No. 3.8e-24;
Matches 470; Conserv. 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 MTSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60
Db 1 MTSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60

Qy 61 KMTAGDNQNLFKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 120
Db 61 KMTAGDNQNLFKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 120

Qy 121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180
Db 121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180

Qy 181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240
Db 181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240

Qy 241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300
Db 241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300

Qy 301 AHSHAVRATORGTOKSIIHTSEDGKVQTRPQARMIRAKLTIVLIVVLIICMGPILL 360
Db 301 AHSHAVRATORGTOKSIIHTSEDGKVQTRPQARMIRAKLTIVLIVVLIICMGPILL 360

Qy 361 AIMYYDVFGRMNKLKITVAFCSMLCLNSTVAPIYALRSKDRLHAFRSMPSCBGTAAQ 420
Db 361 AIMYYDVFGRMNKLKITVAFCSMLCLNSTVAPIYALRSKDRLHAFRSMPSCBGTAAQ 420

Qy 421 PLDNSMGSDCLKHANNAASVRAEESCIKSTVKIAKVTMSVSTDISAEAL 472
Db 421 PLDNSMGSDCLKHANNAASVRAEESCIKSTVKIAKVTMSVSTDISAEAL 472

Qy 1 MTSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60
Db 1 MTSILDGLADTFRTITDLYGSNDIQYEDIKGDMASKLGYFPQKEPLTSFRGSPFQE 60

Qy 61 KMTAGDNQNLFKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 120
Db 61 KMTAGDNQNLFKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 120

Qy 121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180
Db 121 VLSITLGFTVLENLIVCVILNRSLSRCPSTHPIGSLAVADLGSWIVTYSFIDPVF 180

Qy 181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240
Db 181 HRKDSRNVLFLKLGTVIATFTASVGSFLPTATARYISHRPLAYERITVTRPKAVAFCLM 240

Qy 241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300
Db 241 WTAIVIAVLPLIGWCNCKLQSICSDIIPHIDETYLWIGTSVLLFIVTAYAMYIWK 300

Db	241 WTIAVIVAVPLLGNCIEKLSQSVCSDFIPIHIDETYLWIGTVSYLLFIVAYMYILWK 300	Qy	61 KMTAGDNIPOLVPADQVNITEFYNKSLSSPKENEENIQCCENMFDIECEMVNLNPSCQOLATA 120
Qy	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMAIRLAKTLYLILWLLICWGPIL 360	Db	61 KMTAGDNIPOLVPADQVNITEFYNKSLSSPKENEENIQCCENMFDIECEMVNLNPSCQOLATA 120
Db	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMDIRLAKTLYLILWLLICWGPIL 360	Qy	121 VLSLTGTFVLEVLVLCVILHSSRLCRPSYHPIGLAVADLIGSVITYSPIDAEVF 180
Qy	361 AIMYDVFGRKMKLKTVPACFSMCLLNSTVNPIIYALRSKDLRHPASMFPSCEGTAQ 420	Db	121 VLSLTGTFVLEVLVLCVILHSSRLCRPSYHPIGLAVADLIGSVITYSPIDAEVF 180
Db	361 AIMYDVFGRKMKLKTVPACFSMCLLNSTVNPIIYALRSKDLRHPASMFPSCEGTAQ 420	Qy	181 HRKDSRNVLFLKGCGVITASFTASYGSLSLFTIAARYTISIRPLAYKRVTRPKAVVAFCLM 240
Qy	421 PLDNMSGDSDCLKHANNAASVHRAESCIKSTVKIAKTMVSVDTSAAEL 472	Db	181 HRKDSRNVLFLKGCVTASFTASYGSLSLFTIAARYTISIRPLAYKRVTRPKAVVAFCLM 240
Db	421 PLDNMSGDSDCLKHANNAASVHRAESCIKSTVKIAKTMVSVDTSAAEL 472	Qy	241 WTIATVIAVPLLGNCIEKLSQSVCSDFIPIHIDETYLWIGTVSYLLFIVAYMYILWK 300
Db	241 WTIATVIAVPLLGNCIEKLSQSVCSDFIPIHIDETYLWIGTVSYLLFIVAYMYILWK 300	Db	241 WTIATVIAVPLLGNCIEKLSQSVCSDFIPIHIDETYLWIGTVSYLLFIVAYMYILWK 300
Qy	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMAIRLAKTLYLILWLLICWGPIL 360	Qy	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMAIRLAKTLYLILWLLICWGPIL 360
Db	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMDIRLAKTLYLILWLLICWGPIL 360	Db	301 AHSHAVRMIQRTGQTSIIHTSDBQKVQTRPQDARMDIRLAKTLYLILWLLICWGPIL 360
AC	ADL15025;	Qy	361 AIMYDVFGRKMKLKTVFACFSMCLLNSTVNPIIYALRSKDLRHFASRMFPSCSEGTAQ 420
XX		Db	361 AIMYDVFGRKMKLKTVFACFSMCLLNSTVNPIIYALRSKDLRHFASRMFPSCSEGTAQ 420
DT	06-MAY-2004 (first entry)	XX	
DB	Human CB1 cannabinoid receptor protein for cancer treatment.	DB	421 PLDNMSGDSDCLKHANNAASVHRAESCIKSTVKIAKTMVSVDTSAAEL 472
XX		Qy	421 PLDNMSGDSDCLKHANNAASVHRAESCIKSTVKIAKTMVSVDTSAAEL 472
KW	cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;	Db	
KW	prognosis; mantle cell lymphoma; cancer.	OS	
XX	Homo sapiens.	RESULT 7	
OS		ADN38918	
XX	WO2003068268-A2.	ID	ADN38918 standard; protein; 472 AA.
XX	21-AUG-2003.	XX	
XX	13-FBB-2003; 2003WO-EP001461.	AC	ADN38918;
PP		XX	
PR	14-FEB-2002; 2002GB-00003480.	DT	17-JUN-2004 (first entry)
PR	29-JUN-2002; 2002GB-00015095.	XX	
XX	(BIO1-) BIOINVENT INT AB.	DB	Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:236.
XX	Ek S., Borrebaek CAK, Bhinger M;	XX	Human; differential expression; cancer; angiogenic disorder;
XX	WPI: 2003-697496/66.	XX	KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
DR	DR-N-PSD; ADL15025.	XX	KW inflammatory disease; autoimmune disease;
XX	New compound for treating, imaging, diagnosing or prognosis mantle cell	DB	KW retinal neovascularization syndrome; scarring; uterine fibroid;
PT	PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a	XX	KW detection; diagnosis; prognosis; drug screening; drug targeting;
PT	PT protein (e.g. human autotoxin polypeptide), and a further moiety (e.g.	XX	KW wound healing; contraception; cytostatic; cardiotonic; immunomodulatory;
PT	PT nucleic acid).	XX	KW pulmonary; gene therapy; vaccine.
XX	Disclosure: SEQ ID NO 37; 342pp; English.	OS	
PS		XX	
XX	The invention relates to a compound comprising a binding moiety which	PP	13-NOV-2002; 2002WO-US036810.
CC	selectively binds to a protein or polypeptide listed in the specification	XX	
CC	(e.g. human autotoxin polypeptide or human CD4 signal transducer	PR	13-NOV-2001; 2001US-0350666P.
CC	polypeptide), and a further moiety. The compound is useful in medicine or	PR	21-NOV-2001; 2001US-0332646P.
CC	in the treatment, imaging, diagnosis or prognosis of mantle cell	PR	29-NOV-2001; 2001US-0334333P.
CC	lymphomas (MCL). It is used in preparing a medicament for treating MCL, a	PR	03-DEC-2001; 2001US-0335394P.
CC	diagnostic or prognostic agent for NCL, or an agent for imaging MCL cells	PR	14-DEC-2001; 2001US-0340316P.
CC	in the body of an individual. This sequence corresponds to one of the	PR	08-JAN-2002; 2002US-0347211P.
CC	polypeptides of the invention.	PR	08-JAN-2002; 2002US-0347349P.
XX	Sequence 472 AA;	PR	08-FEB-2002; 2002US-0355280P.
SQ		PR	13-FEB-2002; 2002US-0356714P.
CC	The invention relates to a compound comprising a binding moiety which	PR	2002US-0359077P.
CC	selectively binds to a protein or polypeptide listed in the specification	PR	29-MAR-2002; 2002US-036889P.
CC	(e.g. human autotoxin polypeptide or human CD4 signal transducer	PR	04-APR-2002; 2002US-0370110P.
CC	polypeptide), and a further moiety. The compound is useful in medicine or	PR	12-APR-2002; 2002US-0372246P.
CC	in the treatment, imaging, diagnosis or prognosis of mantle cell	PR	05-JUN-2002; 2002US-0386614P.
CC	lymphomas (MCL). It is used in preparing a medicament for treating MCL, a	PR	16-JUL-2002; 2002US-0396839P.
CC	diagnostic or prognostic agent for NCL, or an agent for imaging MCL cells	PR	22-JUL-2002; 2002US-039775P.
CC	in the body of an individual. This sequence corresponds to one of the	PR	22-JUL-2002; 2002US-039785P.
XX	polypeptides of the invention.	PR	09-SEP-2002; 2002US-0409450P.
Qy	1 MKSILDGLADTFRTITDLYVGNSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSFQE 60		
Db	1 MKSILDGLADTFRTITDLYVGNSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSFQE 60		

(EBSB-) EOS BIOTECHNOLOGY INC. ID ABO60051 standard; protein; 472 AA.

X ID ABO60051 standard; protein; 472 AA.

X XX

I Afar D, Aziz N, Ginesburg WM, Gish KC, Glynn R, Hevezi PA; AC ABO60051;

I Mack DH, Murray R, Watson SR, Wilson KB, Zlotnik A; AC ABO60051;

I WPI; 2003-468649/4. DT 29-JUL-2004 (first entry)

I N-PSDB; ADN38917. XX Human genome derived single exon probe #6285.

I X Determining the presence or absence of a pathological cell in a patient, useful for diagnosing, prognosis or treating cancer, comprises detecting a nucleic acid in a biological sample. XX Human genome expression; single exon probe; microarray; alternative splicing event; genomic alteration.

I X Claim 12: SEQ ID NO 236; 1385pp; English. XX Homo sapiens.

I S The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a pathological cell in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosis and treating cancer and other conditions such as psoriasis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularization syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention. XX Human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

I S Claim 12: SEQ ID NO 236; 1385pp; English.

I S The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid probes for measuring human gene expression (comprising a plurality of single exon nucleic acid probes cited above, where each of the plurality of probes is separately conjugated amino acids of any of the above-mentioned amino acid and addressable isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of measuring human gene expression, a vector comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above-mentioned amino acid sequences (optionally with conservative amino acid substitutions), an isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above). The probe, methods and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising gross alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe protein of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/Sequence.html?DocID=20030194704

I Q Sequence 472 AA;

I Q Query Match 99.5%; Score 2412; DB 7; Length 472; Best Local Similarity 99.6%; Prod. No. 3.be-247; Indels 0; Gaps 0; Matches 470; Conservative 0; Mismatches 2; Gaps 0;

I Y 1 MKSLDGLADTFTRITIDLLYGSNDIQQEDTKDMASKLGYFPQKEPLTSRGSFQQ 60
I Y 1 MKSLDGLADTFTRITIDLLYGSNDIQQEDTKDMASKLGYFPQKEPLTSRGSFQQ 60

I Y 61 KMTAGDNQLPVQDPQNITEFYKNSKLSSPKENENIQGENFMNDIECFMVLNPSQLATA 120
I Y 61 KMTAGDNQLPVQDPQNITEFYKNSKLSSPKENENIQGENFMNDIECFMVLNPSQLATA 120

I Y 61 KMTAGDNQLPVQDPQNITEFYKNSKLSSPKENENIQGENFMNDIECFMVLNPSQLATA 120

I Y 121 VLSLTGFTPVLENLIVLHSLSRQCRSPTHFPGSLAVDILGSVTFVSPIDFMPV 180
I Y 121 VLSLTGFTPVLENLIVLHSLSRQCRSPTHFPGSLAVDILGSVTFVSPIDFMPV 180

I Y 181 HRKDSRAVNFVFLKGIGTASFTAVGSPLTATARYISITHRPLAYKRTVRKAVAFCLM 240
I Y 181 HRKDSRAVNFVFLKGIGTASFTAVGSPLTATARYISITHRPLAYKRTVRKAVAFCLM 240

I Y 241 WTAIAVIAVPLIGWNCERKLOQSYCSDFIPPHIDETYLTMIGTVSLLFIVYAYMYILWK 300
I Y 241 WTAIAVIAVPLIGWNCERKLOQSYCSDFIPPHIDETYLTMIGTVSLLFIVYAYMYILWK 300

I Y 241 WTAIAVIAVPLIGWNCERKLOQSYCSDFIPPHIDETYLTMIGTVSLLFIVYAYMYILWK 300

I Y 301 AHSHAVRM1QRGTQSKLIIHTSEDGKVYOTRPGDARMARLAKTLVLLVLLICWGPFL 360
I Y 301 AHSHAVRM1QRGTQSKLIIHTSEDGKVYOTRPGDARMARLAKTLVLLVLLICWGPFL 360

I Y 361 AIMVYDVGKMNKLKITYFAFCMSMCILUNSTNPVIIYARSKDOLRAHFSMPPSCEGTAAQ 420
I Y 361 AIMVYDVGKMNKLKITYFAFCMSMCILUNSTNPVIIYARSKDOLRAHFSMPPSCEGTAAQ 420

I Y 420 PLDNSMGDSCLHKHANNAASVRAAESCKSTVKIARTMSYSTDTSAEAL 472
I Y 420 PLDNSMGDSCLHKHANNAASVRAAESCKSTVKIARTMSYSTDTSAEAL 472

I Y 421 PLDNSMGDSCLHKHANNAASVRAAESCKSTVKIARTMSYSTDTSAEAL 472
I Y 421 PLDNSMGDSCLHKHANNAASVRAAESCKSTVKIARTMSYSTDTSAEAL 472

Db	241	WTAIVAVLPLIGWCERQSVSDIPPHIDETYLWIK	300	QY	61	KMTAGDNFQLVPADQVNITEFYNSKLSFSKENEENIQGENFMDIECEMVNLNPQQLAIA 120
QY	301	AHSHAVRMQIORTGOKSIINTSEDGKVQTRPDAORMIRLAKTLVLLVLLICMGPILL	360	Db	61	KMTAGDNFQLVPADQVNITEFYNSKLSFSKENEENIQGENFMDIECEMVNLNPQQLAIA 120
Db	301	AHSHAVRMQIORTGOKSIINTSEDGKVQTRPDAORMIRLAKTLVLLVLLICMGPILL	360	QY	121	VLSLTLCPTFTVLENILVLCVTHSRSPCRPSYHFIGSLAVADLGLSYTIFYSFIDPHVF 180
QY	361	AIWYDVFGRMNKLKITYFAFCSMILCLINSTYNPIIYALRSKDLRHSMPSCGEAQ	420	Db	121	VLSLTLCPTFTVLENILVLCVTHSRSPCRPSYHFIGSLAVADLGLSYTIFYSFIDPHVF 180
Db	361	AIWYDVFGRMNKLKITYFAFCSMILCLINSTYNPIIYALRSKDLRHSMPSCGEAQ	420	QY	181	HRKDSRNVLFLKGVTASFTASVGSLPLTAYRISIHRPLAYKRLVTRPKAVAVFCLM 240
QY	421	PLDMSMGSDCLRHANNAASVRAECSKTKVIAKVTMSVSTDIAEAL 472		Db	181	HRKDSRNVLFLKGVTASFTASVGSLPLTALDRYIISIHRPLAYKRLVTRPKAVAVFCLM 240
Db	421	PLDMSMGSDCLRHANNAASVRAECSKTKVIAKVTMSVSTDIAEAL 472		QY	241	WTIAIVAVLPLIGWCERKLSQVCSDFPHIDETYLFWIGTSVLLFIVVAYMLWK 300
				Db	241	WTIAIVAVLPLIGWCERKLSQVCSDFPHIDETYLFWIGTSVLLFIVVAYMLWK 300
				QY	301	AHSHAVRMQIORTGOKSIIHTSGDKYQVTRPDAQMAIRLAKTLVLLVLLICMGPILL 360
				Db	301	AHSHAVRMQIORTGOKSIIHTSGDKYQVTRPDAQMDIRLAKTLVLLVLLICMGPILL 360
AC	AEA81221	standard; protein; 472 AA.		QY	361	AMVYDVFGRMNKLKITYVAFCSMCLINSTYNPIIYALRSKDLRHSMPSCGEAQ 420
XX	XX			Db	361	AMVYDVFGRMNKLKITYVAFCSMCLINSTYNPIIYALRSKDLRHSMPSCGEAQ 420
AC	AEA81221;			QY	421	PLDMSMGSDCLRHANNAASVRAECSKTKVIAKVTMSVSTDIAEAL 472
XX	XX			Db	421	PLDMSMGSDCLRHANNAASVRAECSKTKVIAKVTMSVSTDIAEAL 472
DT	25-AUG-2005	(first entry)				
DS	Human cannabinoid receptor 1 (brain) variant 1 protein.					
XX						
•	KW	screening; obesity; nutritional disorder; anorectic;				
XX						
OS	Homo sapiens.					
PN	US2005136465-A1.					
XX						
PD	23-JUN-2005.					
XX						
PF	22-DEC-2004; 2004US-00019829.					
XX						
PR	22-DEC-2003; 2003EP-00104902.					
XX						
PA	(CLER/) CLERC R G.					
PA	(DUCH/) DUCHATEAU-NGUYEN G.					
PA	(GARD/) GARDES C.					
PA	(MIZR/) MIZRAHI J.					
PA	(OSTE/) OSTENSON C.					
P1	Clerc RG, Duchateau-Nguyen G, Gardes C, Mizzrahi J, Ostenson C;					
XX						
XX	WPI; 2005-457507/46.					
DR	N-PSDB; AEA81160.					
XX						
PR	Screening test compounds that reduce and/or prevent obesity involves contacting cell expressing gene from alpha-two-glycoprotein.					
XX						
PS	Claim 18; SEQ ID NO 88; 21pp; English.					
XX						
CC	The invention relates to a novel method for screening for test compounds that reduce and/or prevent obesity. The method comprises contacting a cell expressing a gene selected from SEQ ID NO. 1-12 or 25-85, with a compound. The method of the invention demonstrates anorectic applications and may be useful for screening for compounds that reduce and/or prevent obesity. The current sequence is that of the human cannabinoid receptor 1 (brain) variant 1 protein of the invention. The sequence listing for the specific specification can be located via the USPTO web-site.					
XX						
CC	Sequence 472 AA;					
SQ	Query Match 99.5%; Score 2412; DB 9; Length 472;					
	Best Local Similarity 99.6%; Pred. No. 3.8e-240;					
	Matches 470; Conservative 0; Mismatches 2; Indels 0; Gap 0;					
QY	1 MKSLIDGLADTTPTITTDLYCGSNDIQEDIKGDMASKLGYPQKPLTSRGSPQE 60					
Db	1 MKSLIDGLADTTPTITTDLYCGSNDIQEDIKGDMASKLGYPQKPLTSRGSPQE 60					

CC present sequence is a non-endogenous version of a known human GPCR
 XX SQ Sequence 472 AA;

Query Match Score 2407; DB 4; Length 472;
 Best Local Similarity 99.4%; Pred. No. 1. 3e-239;
 Matches 469; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKSILDGLADTTFTITDLYVGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFQE 60
 DB 1 MKSILDGLADTTFTITDLYVGSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFQE 60

QY 61 KMTAGCDNPOLYPAQVNTEPFYNKSLSPKENENMIOGENEMDIECMVLNPSQLAIA 120
 DB 61 KMTAGCDNPOLYPAQVNTEPFYNKSLSPKENENMIOGENEMDIECMVLNPSQLAIA 120

QY 121 VLSLTLGTFVLENILVLCVILHSRSLRCPSTHFIGSLAVADLIGSLTIVYSPIDFVFP 180
 DB 121 VLSLTLGTFVLENILVLCVILHSRSLRCPSTHFIGSLAVADLIGSLTIVYSPIDFVFP 180

QY 181 HKDSRNVTELFLKGTVTAESTASGSLSLFTATAARYISIHRPLAYKRITYTRPKAVAFCLM 240
 DB 181 HKDSRNVTELFLKGTVTAESTASGSLSLFTATAARYISIHRPLAYKRITYTRPKAVAFCLM 240

QY 241 WTAIAVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300
 DB 241 WTAIAVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300

QY 301 AHSHAVRMORGTOKSIIHTSEDGVQVTRPDRMAIRLAKTTLVLLVLLICWGPIL 360
 DB 301 AHSHAVRMORGTOKSIIHTSEDGVQVTRPDRMAIRLAKTTLVLLVLLICWGPIL 360

QY 361 AIMYDVFGRMKNLKTKVAFCSMUCLNLSTYNPTIYALRSKDLRHAFSMFPSCBGTQ 420
 DB 361 AIMYDVFGRMKNLKTKVAFCSMUCLNLSTYNPTIYALRSKDLRHAFSMFPSCBGTQ 420

QY 421 PLDSMGSDSCLKHANNAASVHRAESCKSTKVIKATYMSVSTDTSAAEL 472
 DB 421 PLDSMGSDSCLKHANNAASVHRAESCKSTKVIKATYMSVSTDTSAAEL 472

RESULT 12 ADN38920 standard; protein; 472 AA.

ID ADN38920 AC ADN38920; XX DT 17-JUN-2004 (first entry)
 DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:238.
 XX Human; differential expression; cancer; angiogenic disorder;
 KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;
 KW inflammatory disease; autoimmune disease;
 KW retinal neovascularization syndrome; scarring; uterine fibroid;
 KW detection; diagnosis; prognosis; drug screening; drug targeting;
 KW wound healing; Contraception; Cytostatic; cardiotonic; immunomodulatory;
 KW vulnerability; gene therapy; vaccine.
 OS Homo sapiens.
 PN WO2003042661-A2.
 XX PD 22-MAY-2003.
 XX PP 13-NOV-2002; 2002WO-US036810.
 XX PR 13-NOV-2001; 2001US-035066P.
 PR 13-NOV-2001; 2001US-033264P.
 PR 29-NOV-2001; 2001US-033493P.
 PR 03-DEC-2001; 2001US-033594P.
 PR 14-DEC-2001; 2001US-0340276P.
 PR 08-JAN-2002; 2002US-034721P.

PR 10-JAN-2002; 2002US-0347349P.
 PR 08-FEB-2002; 2002US-035250P.
 PR 13-FEB-2002; 2002US-035671P.
 PR 20-FEB-2002; 2002US-035907P.
 PR 04-APR-2002; 2002US-0372246P.
 PR 12-APR-2002; 2002US-0372246P.
 PR 16-JUL-2002; 2002US-038661P.
 PR 22-JUL-2002; 2002US-0397775P.
 PR 22-JUL-2002; 2002US-0397845P.
 PR 09-SEP-2002; 2002US-0409450P.
 XX (EBSB-) EOS BIOTECHNOLOGY INC.
 PA. XX PI Afar D, Aziz N, Ginsburg WM, Gish KC, Glynn R, Hevezi PA,
 Mack DH, Murray R, Watson SR, Wilson KE, Zlotnick A;
 XX WPI; 2003-466649/44.
 DR -N-PSDB; ADN38919.
 XX Claim 12; SEQ ID NO 238; 1385pp; English.
 CC The invention relates to nucleic acids and proteins (ADN38683-ADN40064) whose expression is upregulated or downregulated in specific cancers or other diseases such as angiogenic or fibrotic disorders, and to methods of determining the presence or absence of a nucleic acid in a patient by detecting a nucleic acid at least 80% identical to those of the invention or by detecting a polypeptide of the invention. The invention also relates to expression vectors and host cells comprising a nucleic acid of the invention; antibodies which specifically bind a polypeptide of the invention; use of such antibodies for drug targeting; and methods of screening for modulators of activity or expression of the polypeptides and nucleic acids. The nucleic acids, polypeptides, antibodies and methods are useful for diagnosing, prognosis and treating cancer and other conditions such as porosis, ischaemia, heart disease, atherosclerosis, inflammatory diseases, autoimmune diseases, retinal neovascularization syndromes, scarring and uterine fibroids. They may also be useful in wound healing and in contraception. The present sequence represents a polypeptide of the invention.
 XX SQ Sequence 472 AA;

Query Match Score 2401; DB 7; Length 472;
 Best Local Similarity 98.9%; Pred. No. 5.2e-239;
 Matches 467; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 MKSILDGLADTTFTITDLYVNSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFQE 60
 DB 1 MKSILDGLADTTFTITDLYVNSNDIQYEDIKGDMASKLGYPPQKPLTSFRGSPFQE 60

QY 61 KMTAGDNPOLYPAQVNTEPFYNKSLSPKENENMIOGENEMDIECMVLNPSQLAIA 120
 DB 61 KMTAGDNPOLYPAQVNTEPFYNKSLSPKENENMIOGENEMDIECMVLNPSQLAIA 120

QY 121 VLSLTIGTFVLENILVLCVILHSRSLRCPSTHFIGSLAVADLIGSLTIVYSPIDFVFP 180
 DB 121 VLSLTIGTFVLENILVLCVILHSRSLRCPSTHFIGSLAVADLIGSLTIVYSPIDFVFP 180

QY 181 HRKDSRNVFLFKLGTVTAESTASGSLSLFTATAARYISIHRPLAYKRITYTRPKAVAFCLM 240
 DB 181 HRKDSRNVFLFKLGTVTAESTASGSLSLFTATAARYISIHRPLAYKRITYTRPKAVAFCLM 240

QY 241 WTIATVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300
 DB 241 WTIATVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300

QY 301 WTIATVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300
 DB 301 WTIATVIAVLPILLGNCBQKQSVDIFPHIDETYLMPHIGNTVSYLLPIVYAMYILWK 300

Db	301	AHSHAVRMIQRGTKSIIHTSEDGKVQVTRPDAQMDIRLAKTLVLVLLICWGPLI	360	CC cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a human cosmid library and a positive clone was identified. There is ca. 97 per cent homology between the deduced amino acid sequences of the human and rat cannabinoid receptors. The specification includes the sequence of a cDNA fragment which encodes this rat cannabinoid receptor protein but the copy quality is extremely poor. Recombinantly produced receptor can be used to screen for new drugs suitable for treatment of cannabinoid-treatable conditions, e.g. glaucoma, bronchial asthma, etc. See AAQ14003 and AAR14195 for human cannabinoid receptor sequences. (Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html .) (Updated on 25-MAR-2003 to correct PA field.)
Qy	361	AIMYYDVFERNKLKIKTYFAFCSMCLCNSTYVPIYLRSKDLRHAFRSMPPSCETAQ	420	XX
Db	361	AIMYYDVFERNKLKIKTYFAFCSMCLCNSTYVPIYLRSKDLRHAFRSMPPSCETAQ	420	CC
Qy	421	PLDNMGDSDCLKHANNAASVHRAAESCIKSTVKIAKVTMSYSTDSAAEL	472	CC
Db	421	PLDNMGDSDCLKHANNAASVHRAAESCIKSTVKIAKVTMSYSTDSAAEL	472	CC
RESULT 13				
ID	AAR14195	standard; protein; 473 AA.		
XX				
AC	AAR14195;			
XX				
SQ	Sequence 473 AA:			
		Query Match 96.7%; Score 2343.5; DB 2;		
		Best Local Similarity 96.8%; Pred. No. 4.7e-233;		
		Matches 458; Conservative 5; Mismatches 9;		
		Indels 1; Gaps 1;		
		1 MKSLDGLADTTFRTRITDLYVGNSNDIQYEDIKGDWASKLGXFPKQKPLTSFRGSPEQ 60		
		1 MKSLDGLADTTFRTRITDLYVGNSNDIQYEDIKGDWASKLGXFPKQKPLTSFRGSPEQ 60		
		61 KTAGDNPQLVA-DQVNITEPNKSLSSFKENENIQCGENFMIDECFMYLNPSQQLAI 119		
		61 KTAGDNPQLVA-DQVNITEPNKSLSSFKENENIQCGENFMIDECFMYLNPSQQLAI 120		
		62 AVLSLTLGFTFTYLENLVLCVILHSRSURCRPSYHFIGSLAVADLIGLSVIFTYSFIDFH 179		
		120 AVLSLTLGFTFTYLENLVLCVILHSRSURCRPSYHFIGSLAVADLIGLSVIFTYSFIDFH 179		
		121 AVLSLTLGFTFTYLENLVLCVILHSRSURCRPSYHFIGSLAVADLIGLSVIFTYSFIDFH 180		
		180 FHRKDSRNVLFLKGIGYTAESFTASGSLFLTAAIARYSIHRLPLAYKRVTRPKAVAFCL 239		
		181 FHRKDSRNVLFLKGIGYTAESFTASGSLFLTAAIARYSIHRLPLAYKRVTRPKAVAFCL 240		
		240 MWTHIAIVIAVNLPLGHNCCEKLOSVCSDFPHDETYLMFWIGSYTSMVLLFIVYAYMILW 299		
		241 MWTHIAIVIAVNLPLGHNCCEKLOSVCSDFPHDETYLMFWIGSYTSMVLLFIVYAYMILW 300		
		300 KAHSHAVRMIQRTQKSIIHTTSEDGKVQVTPDQARMAIRLAKTLVLVVLICWGPL 359		
		301 KAHSHAVRMIQRTQKSIIHTTSEDGKVQVTPDQARMDIRLAKTLVLVVLICWGPL 360		
		360 LAIMYDVFGRKNLKIKTVFARCSMLCILNSTVNPIYALRSKDLRHAFRSMPSCEATA 419		
		361 LAIMYDVFGRKNLKIKTVFARCSMLCILNSTVNPIYALRSKDLRHAFRSMPSCEATA 420		
		420 QPLDNMGSDSDCLKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAAEL 472		
		421 QPLDNMGSDSDCLKHANNTASMRAAESCIKSTVKIAKVTMSVSTDTSAAEL 473		
		RESULT 14		
		ADD46381 standard; protein; 473 AA.		
		XX		
		AC ADD46381;		
		XX		
		DT 29-JAN-2004 (first entry)		
		XX		
		DB Rat Protein P202/2, SEQ ID NO 12061.		
		XX		
		KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;		
		KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.		
		XX		
		OS Rattus norvegicus.		
		XX		
		PN WO2003016475-A2.		
		XX		
		PD 27-FEB-2003.		
		XX		
		CC		

PF	14-AUG-2002; 2002RQ-US025765.	Qy	300 KAASHAVRMIGRTQKSIIIIHTSBDGKVQTRPQARMAIRLAKTLYILVVLICWGPL 359
XX		Db	301 KAASHAVRMIGRTQKSIIIIHTSBDGKVQTRPQARMDIRLAKTLYILVVLICWGPL 360
PR	14-AUG-2001; 2001US-0312147P.	Qy	360 LAIMVYDVEKMKNLKTYFAFCMCLLNSTVNPIYALRSKDLRHAFRSMPSCEGTA 419
PR	01-NOV-2001; 2001US-0345382P.	Db	361 LAIMVYDVEKMKNLKTYFAFCMCLLNSTVNPIYALRSKDLRHAFRSMPSCEGTA 420
XX	26-NOV-2001; 2001US-0333347P.	Qy	420 QPLDNMGDSDCIHKHANNAASVRAECKSTVKIAKVTMSVSTDSEAEL 472
PA	(GEHO) GEN HOSPITAL CORP.	Db	421 QPLDNMGDSDCIHKHANNTASHRAECKSTVKIAKVTMSVSTDSEAEL 473
PA	(FARB) BAYER AG.		
XX	Woolf C, D'urso D, Befort K, Costigan M;		
PI	WPI; 2003-268312/26.		
XX	GENBANK; P20272.		
DR			
XX	PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.	RESULT 15	
PT		ABB57048	
XX		ID ABB57048 standard; protein; 473 AA.	
PS	Claim 1; Page; 1017pp; English.	XX	
XX	The invention discloses a composition comprising two or more isolated rat or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polymucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antisera. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.	AC	ABB57048;
XX	Sequence 473 AA;	DT	07-MAR-2002 (First entry)
XX		XX	Mouse ischaemic condition related protein sequence SEQ ID NO:77.
CC		DE	Mouse ischaemic condition
CC		KW	ischaemia; compressive ischaemia; occlusive ischaemia;
CC		KW	vasospastic ischaemia; ischaemic condition; ischaemic disease.
CC		OS	Mus musculus.
CC		PN	WO200188188-A2.
CC		XX	WO200188188-A2.
CC		PR	2000JP-00145977.
CC		XX	XX (UNIV - UNIV NIHON SCHOOL JURIDICAL PERSON.
CC		PA	PA
CC		XX	22-NOV-2001.
CC		PP	18-MAY-2001; 2001WO-JP004192.
CC		XX	XX
CC		PR	18-MAY-2000; 2000JP-00145977.
CC		XX	XX
CC		DR	WPI; 2002-034733/04.
CC		DR	N-PSDB; ABI9249.
CC		XX	XX
CC		PT	Examining the ischemic condition (e.g. occlusive ischæmia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these genes.
CC		PT	PT
CC		PT	determining the expression profile of the present invention
CC		XX	PT
CC		PS	Claim 2; Page 235-237; 2690pp; English.
XX		XX	The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (II) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring expression levels of particular genes (ABI99202 to ABI9912, encoding the protein sequences in AB57020 to AB57374) or by determining the expression profile of a gene group comprising these genes. The expression levels or expression profiles produced by these genes are used as an indicator when screening for ischaemic condition-improving drugs or therapeutics for ischaemic diseases. ABI9913 and ABI9914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention
XX		SQ	Sequence 473 AA;
XX		XX	Sequence 473 AA;
Qy	Query Match 96.7%; Score 2343.5; DB 7; Length 473;	XX	XX
Best Local Similarity 96.8%; Pred. No. 4.7e-233; Indels 1; Gaps 1; Matches 458; Conservative 5; Mismatches 9;	CC	CC	CC
Db	1 MKSILDQGLADTFRTITDLYLGGSNDIQEDIKGDMASKLGYFPKPKPLTSFRGSPFQE 60	CC	CC
Qy	61 KMTAGDNQOLPA-DQVNITEPYKNSLSSPKNEENIQGENFMIDECFMVNLNPSQLAI 119	CC	CC
Db	61 KMTAGDNQPLVAGDTTNTEPYKNSLSSPKNEENIQGENFMIDECFMVNLNPSQLAI 120	CC	CC
Qy	120 AVLSLTGTTGTFLVLENLVLVLYLTCYLHSRSLRCPSYHFTGSLAVADLIGSVIFVYSFDFHV 179	CC	CC
Db	121 AVLSLTGTTGTFLVLENLVLVLYLTCYLHSRSLRCPSYHFTGSLAVADLIGSVIFVYSFDFHV 180	CC	CC
Qy	180 FHRKDSSENVLFPLKGCCATASFTAVSGSLFLTAIARYSISHRPLAYKRIVTRPKAVVFC 239	CC	CC
Db	181 FHRKDSNVLFPLKGCCATASFTAVSGSLFLTAIDRISHRPLAYKRIVTRPKAVVFC 240	CC	CC
Qy	240 MWTIAIVIAVLPPLGNNECEKLSQCVSCSDIPHDIDETYLFWIGTVTSVLLFIVYATMYILW 299	CC	CC
Db	241 MWTIAIVIAVLPPLGNNECEKLSQCVSCSDIPHDIDETYLFWIGTVTSVLLFIVYATMYILW 300	CC	CC
Qy	1 MKSILDQGLADTFRTITDLYVGNSNDIQEDIKGDMASKLGYFPKPKPLTSFRGSPFQE 60	CC	CC

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Db      1 MKSILDGLADTTFTTITDLYGSNDIQYEDIKGDMASKLGYPPQKEPLTSFRGSPFQE 60
Qy      61 KMTAGDNPOLYPA-DVNNITEFTNKSLSFKENENICOGENFMDEKEMVNPSQQLAI 119
Db      61 KMTAGDNSPLVPGADTTITEFTNKSLSFKENEDNICOGENFMDEKEMVNPSQQLAI 120
Qy      120 AVSLTLLGPTVLENLIVCILHRSRSCRPSPYHFIGSLAVADLSSVIFTYSPIDFHV 179
Db      121 AVSLTLLGPTVLENLIVCILHRSRSCRPSPYHFIGSLAVADLSSVIFTYSPIDFHV 180
Qy      180 FHRKDSRVNVLFLKGGVTASFTAVSGSLFLTAARYISIIRPLAYKRVTRPKAVAFCL 239
Db      181 FHRKDSPVNVLFLKGGVTASFTAVSGSLFLTAFLDRYISIIRPLAYKRVTRPKAVAFCL 240
Qy      240 MWTTAIVAVPLIGWNCVKLQSVCSDPFIIDETYLFWIGTVSULLFITYAYMILW 299
Db      241 MWTTAIVAVPLIGWNCVKLQSVCSDPFIIDETYLFWIGTVSULLFITYAYMILW 300
Qy      300 KAISHAVMIQRTQKSIIHTSEDGVQVTRDDQANAIRLAKTLVILVVLICGPL 359
Db      301 KAISHAVMIQRTQKSIIHTSEDGVQVTRDDQANDIRLAKTLVILVVLICGPL 360
Qy      360 LAIMVYDFGKMKLIKTVFAFCSMLCILNSTNPITIYALRSKDLRAFRSMFPSCGTAA 419
Db      361 LAIMVYDFGKMKLIKTVFAFCSMLCILNSTNPITIYALRSKDLRAFRSMFPSCGTAA 420
Qy      420 QPLDNMSGDSDCHKHANNAASVRAASCICSTVKAKVTMVSYSTDSABAL 472
Db      421 QPLDNMSGDSDCHKHANNTASMHRRAASCICSTVKAKVTMVSYSTDSABAL 473

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• Search completed: January 6, 2006, 21:08:29
 Job time : 194 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:08:38 ; Search time 13 Seconds
 Perfect score: 2424
 Sequence: 1 MKSILDGLADTTFTRTTIDL.....TVKIAKVTMSVSTDTSAAEL 472

Title: US-10-521-420-1

Scoring table: BLOSUM62
 Gapext 0.5

Searched: 61072 seqs, 8486849 residues

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database : Published Applications AA_New:
 1: /cgn2_6/prodata/2/pubaa/US08_NEW_PUB_pep:
 2: /cgn2_6/prodata/2/pubaa/US06_NEW_PUB_pep:
 3: /cgn2_6/prodata/2/pubaa/US07_NEW_PUB_pep:
 4: /cgn2_6/prodata/2/pubaa/PCT_NEW_PUB_pep:
 5: /cgn2_6/prodata/2/pubaa/US05_NEW_PUB_pep:
 6: /cgn2_6/prodata/2/pubaa/US10_NEW_PUB_pep:
 7: /cgn2_6/prodata/2/pubaa/US11_NEW_PUB_pep:
 8: /cgn2_6/prodata/2/pubaa/US60_NEW_PUB_pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1-1	2412	99.5	472	7	US-11-127-877-39	Sequence 39, Appli
2	710	29.3	360	6	US-10-851-667A-26	Sequence 26, Appli
3	363	15.0	364	7	US-11-067-894-2	Sequence 2, Appli
4	352.5	14.5	378	6	US-10-995-561-891	Sequence 891, App
5	351.5	14.5	382	7	US-11-124-368A-173	Sequence 173, App
6	351.5	14.5	382	7	US-11-124-368A-174	Sequence 174, App
7	351.5	14.5	382	7	US-11-127-877-58	Sequence 58, Appli
8	341	14.1	353	7	US-11-067-894-6	Sequence 6, Appli
9	311.5	12.9	351	7	US-11-067-894-4	Sequence 4, Appli
10	310.5	12.8	334	7	US-11-110-274-6	Sequence 6, Appli
11	289	11.9	330	7	US-11-110-274-4	Sequence 4, Appli
12	283	11.7	466	7	US-11-127-877-51	Sequence 51, Appli
13	283	11.7	466	7	US-11-127-877-50	Sequence 50, Appli
14	280	11.6	362	7	US-11-110-274-5	Sequence 5, Appli
15	272	11.2	360	6	US-10-995-561-547	Sequence 547, Appli
16	248.5	10.3	254	6	US-10-05-877-248	Sequence 248, Appli
17	248.5	10.3	254	6	US-10-05-877-324	Sequence 327, Appli
18	248.5	10.3	254	6	US-10-05-877-340	Sequence 340, Appli
19	235.5	9.7	797	6	US-10-995-561-802	Sequence 802, Appli
20	231.5	9.6	317	6	US-10-995-561-798	Sequence 798, Appli
21	222.8	9.4	318	7	US-11-127-877-38	Sequence 38, Appli
22	222.5	9.2	480	6	US-10-541-162-40	Sequence 40, Appli
23	221	9.1	259	6	US-10-055-877-225	Sequence 225, Appli
24	221	9.1	257	6	US-10-055-877-237	Sequence 237, Appli
25	216.5	8.9	471	6	US-10-995-561-901	Sequence 901, Appli

ALIGNMENTS

RESULT 1
 US-11-127-877-39
 / Sequence 39, Application US/11127877
 / Publication No. US20050281565A1
 / GENERAL INFORMATION:
 / APPLICANT: Merchiers, Pascal G.
 / APPLICANT: Hoffmann, Marcel
 / APPLICANT: Spittaels, Koenraad F. F.
 / APPLICANT: Laenen, Wendy
 / TITLE OF INVENTION: Amyloid-Compounds and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 / FILE REFERENCE: P27 800-B USA
 / CURRENT APPLICATION NUMBER: US/11/127,877
 / CURRENT FILING DATE: 2005-05-12
 / PRIOR APPLICATION NUMBER: 60/570,352
 / PRIOR FILING DATE: 2000-05-12
 / PRIOR APPLICATION NUMBER: 60/603,948
 / PRIOR FILING DATE: 2004-08-24
 / NUMBER OF SEQ ID NOS: 590
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 39
 / LENGTH: 472
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 US-11-127-877-39

Query Match 99.5%; Score 2412; DB 7; Length 472;
 Best Local Similarity 99.6%; pred. No. 6e-199;
 Matches 470; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

Qy 1 MKSLDGLADTTFTTTDLYVGSNDIQYEDIKGDMASKLGYPFQKPLTSFRGSPPQE 60
 Db 1 MKSLDGLADTTFTTTDLYVGSNDIQYEDIKGDMASKLGYPFQKPLTSFRGSPPQE 60

Query Match 99.5%; Score 2412; DB 7; Length 472;
 Best Local Similarity 99.6%; pred. No. 6e-199;
 Matches 470; Conservative 0; Mismatches 2; Indels 0;
 Gaps 0;

Qy 61 KTAGDNPQLVPAQDNQITEPKNSLSSPTEYNKSLSFKEENETQCGENMDFECMVNLNSQQQLAIA 120
 Db 61 KTAGDNPQLVPAQDNQITEPKNSLSSPTEYNKSLSFKEENETQCGENMDFECMVNLNSQQQLAIA 120

Qy 121 VLSLTIGFTFLNLLVLYCILHRSURCRSYHFISGLAVADLLSVIYFSIDPHVF 180
 Db 121 VLSLTIGFTFLNLLVLYCILHRSURCRSYHFISGLAVADLLSVIYFSIDPHVF 180

Qy 181 HRKDSRNVPFLPKGGTTASPTASVGLSLFLTAIRYSIHRLPLAKIVTRPKAVAFCLM 240
 Db 181 HRKDSRNVPFLPKGGTTASPTASVGLSLFLTAIRYSIHRLPLAKIVTRPKAVAFCLM 240

Qy 241 WTIATIVAVLPPLGNGEKLOSSVSDIPPHDTEYLMPWIGTYSVLLFIVAYMLWK 300

RESULT 2

US-10-851-667A-26 Query Match Score: 29.3%

; Sequence 26, Application US/10851667A ; Publication No. US2005026608A1 ; GENERAL INFORMATION: ; APPLICANT: Zimmer, Andreas ; APPLICANT: Karsak, Melihha ; APPLICANT: de Vernejouli, Marie-Christine ; APPLICANT: Bab, Iliai ; APPLICANT: Shoham, Esther ; APPLICANT: Mechoulam, Raphael ; TITLE OF INVENTION: METHODS, KITS AND PHARMACEUTICAL COMPOSITIONS FOR DIAGNOSING, TREATING AND/OR PREVENTING OSTEOFOROSIS ; FILE REFERENCE: 28030 ; CURRENT APPLICATION NUMBER: US/10/851,667A ; CURRENT FILING DATE: 2004-05-24 ; NUMBER OF SEQ ID NOS: 26 ; SOFTWARE: PatentIn version 3.2 ; SEQ ID NO: 26 ; LENGTH: 360 ; TYPE: PRT ; ORGANISM: Homo sapiens ; FEATURE: NAME/KEY: misc_feature ; LOCATION: (63)-(65) ; OTHER INFORMATION: Non-synonymous polymorphism: Gln or Arg ; US-10-851-667A-26

Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 6 VTEANGSKDGLDN-----PKKDMILSPQTKTAVAVLCTIGLSSALENTAV 54 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 138 LCYVILHRSIRCRPSYHFIGSLAVADLIGSIVFYSFIDFHVPHRKDSRNVLNPSSQIAVAVLSTLGTFTVLENV 137 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 55 LYLTLSSEXTRRKSYLFIGSLAGDFASVVPACSFNEHVFGVDKAVFLKGSTV 114 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 198 ASFTAVSGSLPLTARYTISIRPLAYKRIVTRPKAVVAFCLMTIAVIANVPLIGNC 257 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 115 MTTFPASGVSLTAIDRVCLCRPSYHFIGSLAVADLIGSIVFYSFIDFHVPHRKDSRNVLNPSSQIAVAVLSTLGTFTVLENV 197 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 258 EKLQSVCSDFPHIDETVLMFWIGVTSVLLFIVYAYNNYLWKAHSHAVRMTOGTGTSI 317 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 175 -CPRPCSELFPLPDNLSSWILLFIAFESGLIYTICGHVWLKAHOHTA-----SL 223 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 318 LIHTSEDGKVQVRPDDOARMA- -IRLACTKLVLLVLLVLLICMGPILLAINVYDVGKONKLU 375 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

Db 224 SGH-QDRDV----PGMANNRLDYRALKTLGLVAVLWICWFVLAJAHSLATLSSQV 277 Query Match Score: 29.3% ; Best Local Similarity: 45.2% ; Pred. No. 1.26-53 ; Mismatches: 57 ; Indels: 30 ; Gaps: 6 ; Matches: 149 ; Conservatve: 57 ; Mismatches: 94 ; Indels: 30 ; Gaps: 6 ;

RESULT 4

US-10-995-561-891 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 13 QPKFTANNEPOC-----FYNESTAFFYNRSGRHLATE-----WNTVERKLV 52 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 59 QEKMTAGDNPNOLPVADQVNITFEYNYKSLSSPKKENEEENIQCGENFMIDECFMVUNPSQQL 118 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 119 IAVLISLTLGTFVLENLVCILHSISLRCPSYHFIGSLAVADLIGSIVFYSFIDFH 178 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 53 MG-LGITTCIFIMANLUVVMAIYVNRFHF-PIYYLMANLAADFFAGLAFYLMENGT 110 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 179 VFHRKDSRNVLFLKGTYTASFTAVSGSLPLTARYTISIRPLAYKRIVTRPKAVVAFC 238 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 111 PNTRLTVSTWLLRQLDTSTSVAVNLAAERHLTVFMRQLHTRMSNE-RVVVVIV 169 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 239 LMTTIATIYAVLPLGNNCEKLOVSCDFIEPHIDETYLMFWIGVTSVLLFIVYAVMYL 298 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 170 VTMATIYMGATPSGVNCIDENCSNMAPLYSDSTLVWAIFLNLTFFVMMVVLYAHIF 229 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 299 WRAHSHAVRMQIORTQKSLIHTSEDGKVQVTRPDQARMAMIRAKLTYLILVVLICMGP 358 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 230 GTYQRQTIRMRSR-----HSSGPQRNRDT-----MMSSLKTUVLGAFFIICWT 273 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 359 LIATIMVYDFGKRNKLKITVFCMSLCLLNSTVNPIYIALRSKDLRHAFRSMFPSCEGT 418 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 274 GLVLLLUVCCPQCDVL-AYEKFPLIAEFSNAMPNIYIYSDKEMSATFRQIL---C 327 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 419 AQPLDNSMGDSDCIHKHANN-----AASVHRAAESCI 450 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 328 CQSENPTGPTESSDRSASSLNHTILAGVHSNDHSVV 364 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

RESULT 4

US-10-995-561-891 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

Db 278 KKAPAFCSMLCLINMVNTIYALRSGEIR 307 Query Match Score: 363 ; Best Local Similarity: 27.2% ; Pred. No. 5.5e-24 ; Mismatches: 72 ; Indels: 50 ; Gaps: 10 ; Matches: 108 ; Conservatve: 72 ; Mismatches: 167 ; Indels: 50 ; Gaps: 10 ;

RESULT 3

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; NUMBER OF PENDING CLAIMS: 1
; NUMBER OF PENDING DATE: 2004-11-24
; SOFTWARE: PasteSEQ for Windows Version 4.0
; SEQ ID NO: 891
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-995-561-891

Query Match 14.5%; Score 352.5; DB 6; Length 378;
 Best Local Similarity 29.7%; Pred. No. 4.66-23;
 Matches 105; Conservative 61; Mismatches 131; Indels 57; Gaps 13

Qy	121	VLSLTGFTVLENLVLICHLRSRCKPSTFISLAVAUOLGSFLVISPLDRAFT	180
Db	44	VLFPVTCSPVLENLMLVLAIWONKFAHR-MYFPIGNIALCDLLAGIAYKVNLL--MS	99
Qy	181	HRKQ---SRNVNPLFKLGYTASPTAVSGSLPLTIAARYISI--HRPL-AYKRIVTRPKAV	234
Db	100	GKKTFSLSPTVWMLAREGSMFVALAESTCSLLAIALLIERHTTMKRPYDANKR--HRVYPL	157

Qy	235	VAFCLMWTIAIVIAVPLIGWNCXKLOSCSDIPHIDETYLMEWIGTWSVILLE-Y	292
Db	158	IGMC -WLAIFTLGAIPLGWNCXKLNPDCTIPLYSKKYIACISIFTAIVTVLY	215
Qy	293	AYMYLIWKASHAVRMIQRGTKSIIITTSEDGKVQTRPDAQMARIKLTAKLVLYVL	352
Db	216	DPTVENVKSSSP-----KVAHNNSRSRSMALLRTVIVSVF	252

Qy	353	IICGMPPLAIMYDYFGKRNK --- LIKITVAFCCSMCLJNSTVNPITYALRSKDLRHAFR 409
Db	253	IACWSPLFLIDIVACYQAACPFLFKAQWFI - VLAVTNSAMNPVITLASEMRRAFF 310
Qy	410	SMPFSC --- EGTAAQDLSMGEDCLKHANNAAS ----- VRRAAESCI 450
	:	:

PRESENTS

US-11-124-368A-173

Publication No. US20050287559A1

APPLICANT: Michele Cargill

APPLIANCE: James U. Devitt
ADDICTANT: May Take

INVENTION: Genetic Polymorphisms Associated with Disease Susceptibility

FILE REFERENCE: CL001524

CURRENT FILING DATE : 2005-05-09

PRIOR AFFILIATION NUMBER: 00/388,013
PRIOR FILING DATE: 2004-05-07

PRIOR APPLICATION NUMBER: US 68/625,936

NUMBER OF SEQ ID NOS : 21112

SOLARIS 10 RELEASE NOTES

THE JOURNAL OF CLIMATE

ORGANISM: *Homo sapiens*

卷之三

Query Match Local similarity 17.6% Preced. No. 5; 7e-23;

Matches 105; Conservative 6/; Mismatches 125; Index 83; Gaps 13;

68 PQLVP-----ADQVN-----IIEFYN-----KSLSSFKENNEENIQGENFMDIECFMVLI
QY

卷之三

3	PTSVPLVKAHSSVSDYVNYDIIIVRHYNNTGKLNISADKENSIKL-----	47
Db	112 NPSQQLAIAVSLSLTGTFTVLENLYLCVILHSLRCPSTHFGSLAVADLGSVIFV 171	
Qy	48 -----TSVVFILCCFILENIFTVLTIWTKFTH-RPMYTFIGNALSDLLAGVAYT 99	
Db	100 ANLLSGATTYKLTPAQWFIREGSMVALSASVSLAIAERTYITMLKMKLNGNSNNFR 156	
Qy	227 IVTRPKAVVAFLMNTIAIVAVLPPLGWNCEKLQSVCSDIPPHIDETYLMFWIGTSQL 284	
Db	160 LF-----LLISAC-WVSLIILGGPLIMGMNCISALSSCSTVPLYHGHYILFCFTCTVFTLL 214	
Qy	287 LLFIVV-YAMYIILKAHSHA-----VRMIQRTGQKSIIHTSEDGVQVTTRPDQARMA 338	
Db	214 LLSIVLVLYCRIYSLVTRSRRLTRFKRNISAKRSSEKS----- 251	
Qy	339 IRLAKTLYLIVLVLIICWGPILAIIMYDVEGRKRNKLJKTVP-AFCSMILCLNSTVNPII 398	
Db	252 LLALKTIVLVLYSFTAGWPLFTRDVGCKV-KTCIDLFRABEYPLVLAVLNSTGNPII 310	
Qy	397 YALRSCDLRHAFRSMSFPSCE 416	
Db	311 YTLTMKEMRAPIRIMSCCK 330	
RESULT 6		
	US-11-124-368A-174	
	: Sequence 174, Application US/11124368A	
	; Publication No. US20050287559A1	
	; GENERAL INFORMATION:	
	; APPLICANT: Michele Cargill	
	; APPLICANT: James J. Devlin	
	; APPLICANT: May Luke	
	; TITLE OF INVENTION: Genetic Polymorphisms Associated with	
	; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Therefor	
	; FILE REFERENCE: CL001524	
	; CURRENT APPLICATION NUMBER: US/11/124,368A	
	; CURRENT FILING DATE: 2005-05-09	
	; PRIOR APPLICATION NUMBER: US 60/568, 845	
	; PRIOR FILING DATE: 2004-05-07	
	; PRIOR APPLICATION NUMBER: US 60/625, 936	
	; PRIOR FILING DATE: 2004-11-09	
	; NUMBER OF SEQ ID NOS: 21112	
	; SOFTWARE: Fast-SEQ for Windows Version 4.0	
	; SEQ ID NO: 174	
	; LENGTH: 382	
	; TYPE: PRT	
	; ORGANISM: Homo sapiens	
	US-11-124-368A-174	
Qy	Query Match 14.5%; Score 351.5; DB 7; Length 382;	
	Best Local Similarity 27.6%; Prod. No. 5.7e-23;	
Matche_b	105; Conservative 67; Mismatches 125; Gaps 83; Gaps 1	
Db	68 POLVP-----ADQYN---IIEFYN---KSLSSPGENEENIQCGENFMIDECFMVL 11	
Qy	68 -----ADQYN---IIEFYN---KSLSSPGENEENIQCGENFMIDECFMVL 11	
Db	3 PTSVPLVKAHRSSVSDYVNYDIIIVRHYNNTGKLNISADKENSIKL----- 47	
Qy	112 NPSQQLAIAVSLSLTGTFTVLENLYLCVILHSLRCPSTHFGSLAVADLGSVIFV 17	
Db	48 -----TSVVFILCCFILENIFTVLTIWTKFTH-RPMYTFIGNALSDLLAGVAYT 99	
Qy	172 YSPIDFHVHRDKSRNVLFLKGVTASTASVSSLPLTAIARYS-----IIRPLAYKR 22	
Db	100 ANLLSGATTYKLTPAQWFIREGSMVALSASVSLAIAERTYITMLKMKLNGNSNNFR 15	
Qy	227 IVTRPKAVVAFLMNTIAIVAVLPPLGWNCEKLQSVCSDIPPHIDETYLWFWIGTSQL 28	
Db	160 LF-----LLISAC-WVSLIILGGPLIMGMNCISALSSCSTVPLYHGHYILFCFTCTVFTLL 21	
Qy	287 LLFIVV-YAMYIILKAHSHA-----VRMIQRTGQKSIIHTSEDGVQVTTRPDQARMA 33	

RESULT 7
US-11-127-877-58

Query Sequence 58, Application US/11127877
Publication No. US20050288565A1
GENERAL INFORMATION:
APPLICANT: Merchiers, Pascal G.
APPLICANT: Hoffmann, Marcel
APPLICANT: Spittale, Koenraad F. F.
APPLICANT: Laenen, Wendy
TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid Beta Protein Production
FILE REFERENCE: P27 800-B USA
CURRENT APPLICATION NUMBER: US/11/127,877
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: 60/570,352
PRIOR FILING DATE: 2004-05-12
PRIOR APPLICATION NUMBER: 60/603,948
PRIOR FILING DATE: 2004-08-24
NUMBER OF SEQ ID NOS: 590
SOFTWARE: Patentin Ver. 3.3
SEQ ID NO: 58
LENGTH: 382
TYPE: PRT
ORGANISM: Homo sapiens
US-11-127-877-58

Score: 351.5%; DB 7; Length: 382;

Query Match 14.5%; Score: 351.5%; DB 7; Length: 382;
Best Local Similarity: 27.6%; Pred. No: 5.7e-23; Matches: 105; Conservative: 67; Mismatches: 125; Indels: 83; Gaps: 13;

Db 214 LLSIVILYCRYSLVRSRRLTFRKNISKASISSEKS----- 251

Qy 339 IRLAKTLVLLVLIICPLAIIAMVYDFGKONKLITKF--AFCSMLCLNSTVNPNII 396

Db 252 LALLKTVIILSVPIACWPLFLILLVGCKV-KTCDFLFRAYFLVLAVLNSGTNPNII 310

Qy 397 YALRSKDLRHAFRMFSCE 416

Db 311 YLTNKEVRRAFIRIMSSCK 330

RESULT 8
US-11-067-884-6

Query Sequence 6, Application US/11067884
Publication No. US20050261252A1
GENERAL INFORMATION:
APPLICANT: Miller, Duane D.
APPLICANT: Tigray, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Sardar, Vineet M.
APPLICANT: Elrod, Don B.
APPLICANT: Xu, Ruiping
APPLICANT: Baker, Daniel L.
APPLICANT: Wang, Dean
APPLICANT: Lilliom, Karoly
APPLICANT: Fischer, David J.
APPLICANT: Virág, Tamás

Db 214 LLSIVILYCRYSLVRSRRLTFRKNISKASISSEKS----- 251

Qy 339 IRLAKTLVLLVLIICPLAIIAMVYDFGKONKLITKF--AFCSMLCLNSTVNPNII 396

Db 252 LALLKTVIILSVPIACWPLFLILLVGCKV-KTCDFLFRAYFLVLAVLNSGTNPNII 310

Qy 397 YALRSKDLRHAFRMFSCE 416

Db 311 YLTNKEVRRAFIRIMSSCK 330

RESULT 9
US-11-067-884-4

Query Sequence 4, Application US/11067884
Publication No. US20050261252A1
GENERAL INFORMATION:
APPLICANT: Miller, Duane D.
APPLICANT: Tigray, Gabor
APPLICANT: Dalton, James T.
APPLICANT: Sardar, Vineet M.
APPLICANT: Elrod, Don B.
APPLICANT: Xu, Ruiping
APPLICANT: Baker, Daniel L.
APPLICANT: Wang, Dean
APPLICANT: Lilliom, Karoly
APPLICANT: Fischer, David J.
APPLICANT: Virág, Tamás

Db 214 LLSIVILYCRYSLVRSRRLTFRKNISKASISSEKS----- 251

Qy 339 IRLAKTLVLLVLIICPLAIIAMVYDFGKONKLITKF--AFCSMLCLNSTVNPNII 396

Db 252 LALLKTVIILSVPIACWPLFLILLVGCKV-KTCDFLFRAYFLVLAVLNSGTNPNII 310

Qy 397 YALRSKDLRHAFRMFSCE 416

Db 311 YLTNKEVRRAFIRIMSSCK 330

APPLICANT: Nusser, Nora
 TITLE OF INVENTION: LPA RECEPTOR AGONISTS AND ANTAGONISTS AND METHODS OF
 FILE REFERENCE: 20609/305
 CURRENT APPLICATION NUMBER: US/11/067,884
 PRIOR APPLICATION NUMBER: 2005-02-28
 PRIOR FILING DATE: 2005-04-20
 PRIORITY NUMBER: 60/190,370
 PRIOR APPLICATION NUMBER: 09/811,838
 PRIOR FILING DATE: 2000-03-17
 NUMBER OF SEQ ID NOs: 26
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 4
 LENGTH: 351
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-067-884-4

Query Match Score 12.9%; DB 7; Length 351;
 Best Local Similarity 27.0%; Pred. No. 1.3e-19;
 Matches 90; Conservative 60; Mismatches 150; Indels 33; Gaps 10;

Db 81 PYNKSLSPKENEENIQGENFMIDECMVNLNPSSQQLAVLSTLGLFTPEVLENLLVLCV 140
 8 YNETIGFFPNNSKG-----ELSHWRPKDVVVVA-LGTVSVLVLNTLVAA 56

RESULT 11
 US-11-110-274-4
 Sequence 4, Application US/11110274
 Publication No. US2005026502A1
 GENERAL INFORMATION:
 APPLICANT: Merchiers, Pascal G.
 APPLICANT: Hoffmann, Marcel
 APPLICANT: Spittaels, Kenraad F.
 TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
 Amyloid-beta Protein Production
 FILE REFERENCE: P27 697-A USA
 CURRENT APPLICATION NUMBER: US/11/10,274
 CURRENT FILING DATE: 2005-04-20
 PRIORITY NUMBER: US 60/563,661
 PRIORITY FILING DATE: 2004-04-20
 NUMBER OF SEQ ID NOS: 620
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO 4
 LENGTH: 330
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-110-274-4

Query Match Score 11.9%; DB 7; Length 330;
 Best Local Similarity 27.8%; Pred. No. 1e-17;
 Matches 89; Conservative 61; Mismatches 140; Indels 30; Gaps 12;

Db 113 PSQQLAIAVLSLTGLFTPEVLENLLVLCVHSRSCRSYHPSQSLAVADLGSVIFVY 172
 38 PSPKAWDVLICIS-GTLVSENALVAVIYGTGPAPRA-PMEFLVSLAVADLAGLGLV 95

RESULT 10
 US-11-110-274-6
 Sequence 6, Application US/11110274
 Publication No. US2005026502A1
 GENERAL INFORMATION:
 APPLICANT: Merchiers, Pascal G.
 APPLICANT: Hoffmann, Marcel
 APPLICANT: Spittaels, Kenraad F.
 TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
 Amyloid-beta Protein Production
 FILE REFERENCE: P27 697-A USA
 CURRENT APPLICATION NUMBER: US/11/110,274
 PRIOR APPLICATION NUMBER: US 60/563,661
 PRIOR FILING DATE: 2004-04-20
 NUMBER OF SEQ ID NOS: 620
 SOFTWARE: PatentIn version 3.3
 LENGTH: 334
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-11-110-274-6

Query Match Score 12.8%; DB 7; Length 334;
 Best Local Similarity 26.9%; Pred. No. 1.5e-19;
 Matches 83; Conservative 62; Mismatches 115; Indels 49; Gaps 9;

age 6

; TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 ; TITLE OF INVENTION: Amyloid-Beta Protein Production
 ; FILE REFERENCE: P27 800-B USA
 ; CURRENT APPLICATION NUMBER: US/11/127,877
 ; CURRENT FILING DATE: 2005-05-12
 ; PRIOR APPLICATION NUMBER: 60/570,352
 ; PRIOR FILING DATE: 2004-05-12
 ; PRIOR APPLICATION NUMBER: 60/603,948
 ; PRIOR FILING DATE: 2004-08-24
 ; NUMBER OF SEQ ID NOS: 590
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 50
 ; LENGTH: 466
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-127-877-50

RESULT 12
 US-11-127-877-51
 / Sequence 51, Application US/11127877
 / Publication No. US20050287565A1
 / GENERAL INFORMATION:
 ; APPLICANT: Hoffmann, Marcel
 ; APPLICANT: Spittels, Koenraad F. F.
 ; APPLICANT: Laenen, Wendy
 / TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 / TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 / CURRENT APPLICATION NUMBER: US/11/127,877
 / CURRENT FILING DATE: 2005-05-12
 / PRIOR APPLICATION NUMBER: 60/570,352
 / PRIOR FILING DATE: 2004-05-12
 / PRIOR APPLICATION NUMBER: 60/603,948
 / PRIOR FILING DATE: 2004-08-24
 / NUMBER OF SEQ ID NOS: 590
 / SOFTWARE: Patentin version 3.3
 / SEQ ID NO: 51
 / LENGTH: 429
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 ; US-11-127-877-51

Query Match 11.7%; Score 283; DB 7; Length 466;
 Best Local Similarity 26.2%; Pred. No. 5.2e-17;
 Matches 95; Conservative 72; Mismatches 156; Indels 40; Gaps 12;

Qy 111 LNPSQQLAAAVSLTGTFLENLVLICVILHSSRLCRPSYHTFGLSVAAD-LIGSVI 169
 Db 21 VNISPAAILGIVLGVNLVLISVACRHLH-SVTHYTVNLAVADLLSTV 79

Qy 110 FVYSPIDFHVFHRKDSRNVLFLKGGV-TASPTAVGSLETFATARYISIHFPLAKRIV 228
 Db 80 LPFSAI-FEVLYNAGFRVFCNIMAAVDVLCCCTASIMGLCTISDRTYIGSYPLRPTIV 138

Qy 111 TRPKAVAVPCLMWTIAVAVPLIGWN--CEKLOSVCS-----DIPHIDETYLFW 279
 Db 139 TQRGLMALLCIVWALSLVSIQPLFGWRQAPADETICQNEEPGVVLFSALGSFL--- 195

Qy 112 IGTVSLLFIVYAYMTLWKAHSHAVRMQR----GTQKSIIIIHTSE---DGKVQVTR 331
 Db 229 TRPKAVAVPCLMWTIAVAVPLIGWN--CEKLOSVCS-----DIPHIDETYLFW 279

Qy 113 PLAITLVMCRVTIVAKRESRGLKSGLTDKSDSEQVTIRHKRNAAGPGSMASA 251
 Db 139 TQRGLMALLCIVWALSLVSIQPLFGWRQAPADETICQNEEPGVVLFSALGSFL--- 195

Qy 114 IGTVSLLFIVYAYMTLWKAHSHAVRMQR----GTQKSIIIIHTSE---DGKVQVTR 331
 Db 196 ---PLAITLVMCRVTIVAKRESRGLKSGLTDKSDSEQVTIRHKRNAAGPGSMASA 251

Qy 115 PDQARMAIRL-----AKTLVLLVVLICWGPLIAIMYDVFGKMKLJKTVFAFC 382
 Db 252 KTKTTHFSVRLKPSREKKAATLGIVVGCFVLWLPFLMPIGSFEDFKPFBETVKIV 311

Qy 116 SMCLCNSTNPPIIYALRSKDLRHAFRSMP--SCEGTAQPDNSMGDSDCLHKHANRAS 441
 Db 312 FWLGYLNSCINPIIYPCSSQEFKAFQVNLRIQCLRQSKHALGXT--LHPSSOAVEG 369

Qy 117 SMCLCNSTNPPIIYALRSKDLRHAFRSMP--SCEGTAQPDNSMGDSDCLHKHANRAS 441
 Db 442 VHR 444
 Qy 118 SMCLCNSTNPPIIYALRSKDLRHAFRSMP--SCEGTAQPDNSMGDSDCLHKHANRAS 441
 Db 370 QHK 372

RESULT 14
 US-11-110-274-5
 / Sequence 5, Application US/11110274
 / Publication No. US20050266502A1

; GENERAL INFORMATION:
 ; APPLICANT: Merchiers, Pascal G.
 ; APPLICANT: Hoffmann, Marcel
 ; APPLICANT: Spittels, Koenraad F. F.
 / TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 / FILE REFERENCE: P27 697-A USA
 / CURRENT APPLICATION NUMBER: US/11/110,274
 / CURRENT FILING DATE: 2005-04-20
 / PRIOR APPLICATION NUMBER: US 60/563,661
 / NUMBER OF SEQ ID NOS: 620
 ; SOFTWARE: Patentin version 3.3
 ; SEQ ID NO: 5
 ; LENGTH: 362
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-11-110-274-5

RESULT 13
 US-11-127-877-50
 / Sequence 50, Application US/11127877
 / Publication No. US20050287565A1
 / GENERAL INFORMATION:
 ; APPLICANT: Hoffmann, Pascal G.
 ; APPLICANT: Merchiers, Marcel
 ; APPLICANT: Spittels, Koenraad F. F.
 ; APPLICANT: Hoffmann, Marcel
 ; APPLICANT: Spittels, Koenraad F. F.
 / TITLE OF INVENTION: Methods, Compositions and Compound Assays For Inhibiting Amyloid-Beta Protein Production
 / FILE REFERENCE: P27 697-A USA
 / CURRENT APPLICATION NUMBER: US/11/110,274
 / CURRENT FILING DATE: 2005-04-20
 / PRIOR APPLICATION NUMBER: US 60/563,661
 / NUMBER OF SEQ ID NOS: 620

Query Match 11.6%; Score 280; DB 7; Length 362;
 Best Local Similarity 27.6%; Pred. No. 6.8e-17;
 Matches 89; Conservative 55; Mismatches 112; Indels 66; Gaps 14;

Qy 121 VLSLTLGFTVLENTLVCYLHSRSRIRCRPSYHFIGSLAVADIL--GSVI-FVYSPTID 176
 Db 77 VLLCGSGTVIAGENALVALIASTALAR-TPMFLVGLSLATDILAGGLILHVFQVL- 134

Qy 177 FHVFRKDSPEVNLFLKGGTASFTASVGSLFLTALARISITHRPLAYKRIVTRPKAVVA 236
 Db 135 -----VPSERTVSLTGTGFLVAVASPSSILAITVDRYLSLYNALTYSRRTLGVHIL 188

Qy 237 PCLMFTIATIVAVLPGLGNCCEKLOSVCSDIFF---HIDETYLMEWIGTSVILLFIVY 292
 Db 189 LARITVSLIGLIPVGNRCLAEFAACSVRPLARSHVALLSAAFF-----MVEGM 241

Qy 293 AVMY----TIIKAHSHAVRMIOREGTQKSIIHTSEDGKVQTRPDQARMARIAIRAKTLVL 347
 Db 242 LHLYTRICQVWR-HAHQIALQQ-----HCLAPHLAATR-----KGVTGLAV 283

Qy 348 ILVVLICWGPBLAIAMVYDYGKVKNKLJIKYTFAFCMSL-CUINSTNPVLIYAFSKDLRH 406
 Db 284 VLGTFGASW---LPPAYTCVVGSHED---PAVYTATLTPATYNMINPIYAFRNQEIOR 338

Qy 407 A-----FRSMFPS 414
 Db 339 AIWLLGCFOSKVPRSRSPS 360

RESULT 15
 US-10-995-561-547
 Sequence 547, Application US/10995561
 Publication No. US2005227054A1
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
 TITLE OF INVENTION: DETECTION AND USES THEREOF
 FILE REFERENCE: CL001559
 CURRENT APPLICATION NUMBER: US/10/995,561
 CURRENT FILING DATE: 2004-11-24
 NUMBER OF SEQ ID NOS: 85702
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 547
 LENGTH: 360
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-995-561-547

Query Match 11.2%; Score 272; DB 6; Length 360;
 Best Local Similarity 24.8%; Pred. No. 3.3e-16;
 Matches 105; Conservative 64; Mismatches 151; Indels 104; Gaps 16;

Qy 28 IQYEDIKGDMASKLGYPQPKPLTSFR-----GSPFQEOKTAG-DNPQLVP-----72
 Db 3 IKTLYLEGDFV-----PPVSSSPFLRTLLEPOGSALLTANNSCCCLPSVOTLPN 53

Qy 73 -ADQVNITEFPNKSLSKPENEENIQGENFMIDRPMVNLAPSQQLIAVISLTGFTV 131
 Db 54 GSEHLQAPPNSNSSP-----CEOQPTKPEPV-----LSGIVSL 90

Qy 132 LENLTVLVCYLHSRSRIRCRPSYHFIGSLAVADLGSVITYFSFIDFHFR-----182
 Db 91 LENLTVLAVVGNLH-SEMPFLCSLAVADMVSYNSALETIMIAVHSIDLTFEDQF 149

Qy 183 -KDSRNYFLFKGGTASFTASVGSLFLTALARISITHRPLAYKRIVTRPKAVVAFCLMW 241
 Db 150 IQHMDNIF-----DSMICLVSACNLIAIADRYMTFYALRHSTMVREALTIVAIN 206

Qy 242 TIAIVAVLPGLGNCCEKLSQSYCSD1PHIDETYLMEWIGTSVILLFIVYAMYILWKA 301
 Db 207 VCCGVCGVY-FVYSSBESKMIYV-----LITMF---AMMLMIGTLYVHMFRL 253

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Result No.	Query	Score	Match	Length	DB ID	Description
1	P2154 homo sapien	99.5	472	1	CNR1_HUMAN	
2	Q5i83 pan troglod	99.5	472	2	CNR1_PAN	
3	Q9plj4 homo sapien	99.5	472	2	O4PLJ4_HUMAN	
4	Q71SP5_MACMU	99.5	472	2	Q71SP5_MACMU	
5	Q506U9_HUMAN	98.2	471	2	Q506U9_HUMAN	
6	Q4VBM6_HUMAN	98.1	471	2	Q4VBM6_HUMAN	
7	CNR1_RAT	96.7	473	1	CNR1_RAT	
8	P47746 rattus norv	96.6	473	2	P47746_rattus_norv	
9	CNR1_MOUSE	96.6	473	2	CNR1_MOUSE	
10	Q5SF33_MOUSE	96.3	472	1	Q5SF33_MOUSE	
11	CNR1_FELICA	92.8	473	1	CNR1_FELICA	
12	Q5UB37_HUMAN	91.2	439	2	Q5UB37_HUMAN	
13	CNR1_TARCR	85.2	473	1	CNR1_TARCR	
14	P0801M1_XENLA	83.8	470	2	P0801M1_XENLA	
15	Q5JYLS_HUMAN	80.6	411	2	Q5JYLS_HUMAN	
16	Q6W9C6_DRYNI	74.5	363	2	Q6W9C6_DRYNI	
17	Q6W9CO_9RODE	74.4	363	2	Q6W9CO_9RODE	
18	Q6W9C2_PEDCA	74.3	363	2	Q6W9C2_PEDCA	
19	Q6W9B8_9RODE	74.2	361	2	Q6W9B8_9RODE	
20	Q6W9C4_GRAMU	74.0	363	2	Q6W9C4_GRAMU	
21	Q6W9D1_CASCN	73.8	360	2	Q6W9D1_CASCN	
22	Q6W9B9_sicista_tia	73.7	359	2	Q6W9B9_sicista_tia	
23	Q6W9B7_spermophilu	73.7	363	2	Q6W9B7_spermophilu	
24	Q6W9D2_aplodonta	73.7	364	2	Q6W9D2_aplodonta	
25	Q6W9B4_ZAPP	73.4	362	2	Q6W9B4_ZAPP	
26	Q6W9B6_TAMHU	73.2	364	2	Q6W9B6_TAMHU	
27	Q6W9B5_THOBO	73.1	362	2	Q6W9B5_THOBO	
28	Q6W9C8_DIPSP	72.9	361	2	Q6W9C8_DIPSP	
29	Q6W9C7_DIPSA	72.3	359	2	Q6W9C7_DIPSA	
30	Q4RQX1_TEITNG	72.2	468	2	Q4RQX1_TEITNG	
31	Q6W9C9_CHILLA	72.2	362	2	Q6W9C9_CHILLA	

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OM protein - protein search, using sw model

Run on: January 6, 2006, 21:01:17 ; Search time 231 Seconds
1441.599 Million cell updates/sec

Title: US-10-521-420-1
Perfect score: 2424
Sequence: 1 MKSILDGLADTPTRTITDL.....TVKIAKVTMSVSTDTSAAEL 472

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : UniProt 05.80:
1: uniprot_prot:
2: uniprot_trembl:
*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
CNR1_HUMAN STANDARD; PRT; 472 AA.
ID CNR1_HUMAN STANDARD;
AC P2155; Q13949; Q9UNNO;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Cannabinoid receptor 1 (CB1) (CB-R) (CANN6).
GN Name=CNR1; Synonyms=CNR;
OS Homo sapiens (Human).
OC Bivalvata; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI TaxID=9606;
RN [1] _
RN NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RP TISSUE=Brain stem; PMID=1718258;
RC MEDLINE=s2028198; PMID=1718258;
RX Gerard C., Mollereau C., Vassart G., Parmentier M.;
RA "Molecular cloning of a human cannabinoid receptor which is also
expressed in testis";
RT Biochem. J. 219:129-134 (1991).
RL [2] _
RN NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RP TISSUE=Brain stem; PMID=2262478;
RC MEDLINE=s1088303; PubMed=2262478;
RX Gerard C., Mollereau C., Vassart G., Parmentier M.;
RA "Nucleotide sequence of a human cannabinoid receptor CDNA.";
RT Nucleic Acids Res. 18:142-142 (1990).
RL [3] _
RN NUCLEOTIDE SEQUENCE (ISOFORMS LONG AND SHORT).
RP TISSUE=Lung; PMID=9181329; PubMed=9181329; DOI=10.1074/jbc.270.8.3726;
RC Shire D., Carillon C., Kaghad M., Calandra B., Rinaldi-Carmona M.,
RA Le Fur G., Caput D., Ferrara P.;
RA Kathmann M.; Schlicher B.;
RT "An amino-terminal variant of the central cannabinoid receptor
resulting from alternative splicing.";
RL J. Biol. Chem. 270:3726-3731(1995).
RN [4] _
RN NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RP TISSUE=Hippocampus; PMID=107412; PubMed=107412;
RC Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RA Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RL [5] _
RN NUCLEOTIDE SEQUENCE (ISOFORM LONG).
RP Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RA Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN [6] _
RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM LONG).
RP Kopatz S.A., Aronstam R.S., Sharma S.V.;
RA "cDNA clones of human proteins involved in signal transduction
sequenced by the Guthrie cDNA resource center (www.cdra.org)." ;
RT Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN [7] _

1 MKSILDGLADTPRTITDILYGSNDIQYEDIKGDMASKLGYPQKPLTSFRGSPQQE 60
 1 MKSILDGLADTPRTITDILYGSNDIQYEDIKGDMASKLGYPQKPLTSFRGSPQQE 60
 Db 61 KMTAGDNPOLVPADDNITEFYNSLSSXENEENIQGENFNDIECPMVNFSQQLAIA 120
 Qy 61 KMTAGDNPOLVPADDNITEFYNSLSSXENEENIQGENFNDIECPMVNFSQQLAIA 120
 Db 121 VLSLTIGTFTVLENLVLCLHRSLSRCPSTHEFIGSLAVADLIGSVIFVYSPIDFHFV 180
 Qy 121 VLSLTIGTFTVLENLVLCLHRSLSRCPSTHEFIGSLAVADLIGSVIFVYSPIDFHFV 180
 Db 181 HKDSRNVFELKLGTYTASTASVCSLFLTIAARYSIHRPLAYKRIVTRPKAVAFCLM 240
 Qy 181 HKDSRNVFELKLGTYTASTASVCSLFLTIAARYSIHRPLAYKRIVTRPKAVAFCLM 240
 Db 181 HKDSRNVFELKLGTYTASTASVCSLFLTIAIRDTSIRPLAYKRIVTRPKAVAFCLM 240
 Qy 241 WTAIVAVLPLIGNCVKLQSVCSDIPHIDEYLTMFWIGVTSVLLPFIYAYMLWIK 300
 Db 241 WTAIVAVLPLIGNCVKLQSVCSDIPHIDEYLTMFWIGVTSVLLPFIYAYMLWIK 300
 Qy 301 AHSHAVRMIGRGTOKSIIHTTSRDKQVQTRPDQARMARLAKTLVLLVVLICWGPQL 360
 Db 301 AHSHAVRMIGRGTOKSIIHTTSRDKQVQTRPDQARMARLAKTLVLLVVLICWGPQL 360
 Qy 361 AIMYDVGKRNKLKTVFAPCSMCLLNLNSTVNPPIYAIRSKDLRHAESMFPSCEGTAQ 420
 Db 361 AIMYDVGKRNKLKTVFAPCSMCLLNLNSTVNPPIYAIRSKDLRHAESMFPSCEGTAQ 420
 Qy 421 PLDMSMGDSCLHKHANNAASVRAAESCIKSTVKIAKTMVSVDTSAAEL 472
 Db 421 PLDMSMGDSCLHKHANNAASVRAAESCIKSTVKIAKTMVSVDTSAAEL 472

RESULT 2
 CNRL_PANTR_PANTR STANDARD PRT; 472 AA.
 ID Q51S3;,
 AC Q51S3;,
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cannabinoid receptor 1 (CB1) (CB-R).
 GN Name=CNRL;
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Pan.
 NCBI_TaxID=9598;

OX [1]
 RP NUCLEOTIDE SEQUENCE [MRNA]
 RX PubMed=1520360, DOI=10.1016/j.cell.2004.11.040;
 RA Dorus S., Vallender E.J., Evans P.D., Anderson J.R., Gilbert S.L.,
 RA Mahowald M., Wyckoff G.J., Malcom C.M., Lahn B.T./
 RT "Accelerated evolution of nervous system genes in the origin of Homo
 sapiens";
 RL Cell 119:1027-1040 (2004).
 CC -1 FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by
 CC inhibiting adenylyl cyclase. Could be a receptor for anandamide
 CC (By similarity).
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1 SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC
 DR EMBL; AY66255; AA74293 1; -; mRNA.
 DR InterPro; IPR002230; Cnbind_receptor.
 DR InterPro; IPR000810; Cnoid_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR PANTHER; PTM19266; SP8; Cnoid_receptor1; 1.
 DR Pfam; PF00001; 7em_1; 1.

DR PRINTS; PRO0522; CANABINOIDR.
 DR PRINTS; PRO0562; CANNABINOIDR.
 DR PRINTS; PRO0537; GPROTEIN_RECEP_F1; 1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1; 1.
 DR PROSITE; PS5262; G_PROTEIN_RECEP_F1; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 FT TOPO_DOM 1 116 Extracellular (Potential).
 FT TRANSMEM 1 117 1 (Potential).
 FT TOPO_DOM 1 142 1 (Potential).
 FT TRANSMEM 1 143 154 Cytoplasmic (Potential).
 FT TRANSMEM 1 155 175 2 (Potential).
 FT TOPO_DOM 1 176 187 Extracellular (Potential).
 FT TRANSMEM 1 188 212 3 (Potential).
 FT TOPO_DOM 213 232 Cytoplasmic (Potential).
 FT TRANSMEM 213 233 4 (Potential).
 FT TOPO_DOM 233 255 4 (Potential).
 FT TRANSMEM 233 256 273 Extracellular (Potential).
 FT TRANSMEM 274 299 5 (Potential).
 FT TOPO_DOM 300 344 Cytoplasmic (Potential).
 FT TRANSMEM 345 365 6 (Potential).
 FT TOPO_DOM 366 377 Extracellular (Potential).
 FT TRANSMEM 378 399 7 (Potential).
 FT TRANSMEM 400 472 Cytoplasmic (Potential).
 FT CARBOHYD 77 N-Linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 83 N-Linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 472 AA; 52858 MW; 102E49061D12ABF2 CRC64;
 Query Match 99.5%; Score 2412; DB 1; Length 472;
 Best Local Similarity 99.6%; Pred. No. 2.8e-156;
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1 MKSLTDGLADTPRTITDILYGSNDIODEDIKDMASKLGYPQKPLTSFRGSPFQEQ 60
Db	1 MKSLTDGLADTPRTITDILYGSNDIODEDIKDMASKLGYPQKPLTSFRGSPFQEQ 60

Qy 61 KMTAGDNPOLVPADDNITEFYNSLSSPCKENENIQGENFMDIECPMVNFSQQLAIA 120
 Db 61 KMTAGDNPOLVPADDNITEFYNSLSSPCKENENIQGENFMDIECPMVNFSQQLAIA 120
 Qy 121 VLSLTIGTFTVLENLVLCLHRSLSRCPSTHEFIGSLAVADLIGSVIFTYSPIDFHFV 180
 Db 121 VLSLTIGTFTVLENLVLCLHRSLSRCPSTHEFIGSLAVADLIGSVIFTYSPIDFHFV 180
 Qy 181 HRKDSRNVLFKLGTYTASTASVCSLFLTIAIRDTSIRPLAYKRIVTRPKAVAFCLM 240
 Db 181 HRKDSRNVLFKLGTYTASTASVCSLFLTIAIRDTSIRPLAYKRIVTRPKAVAFCLM 240
 Qy 241 WTIAIVAVLPLIGNCVKLQSVCSDIPHIDEYLTMFWIGVTSVLLPFIYAYMLWIK 300
 Db 241 WTIAIVAVLPLIGNCVKLQSVCSDIPHIDEYLTMFWIGVTSVLLPFIYAYMLWIK 300
 Qy 301 AHSHAVRMIGRGTOKSIIHTTSRDKQVQTRPDQARMARLAKTLVLLVVLICWGPQL 360
 Db 301 AHSHAVRMIGRGTOKSIIHTTSRDKQVQTRPDQARMARLAKTLVLLVVLICWGPQL 360
 Qy 361 AIMYDVGKRNKLKTVFAPCSMCLLNLNSTVNPPIYAIRSKDLRHAESMFPSCEGTAQ 420
 Db 361 AIMYDVGKRNKLKTVFAPCSMCLLNLNSTVNPPIYAIRSKDLRHAESMFPSCEGTAQ 420
 Qy 421 PLDMSMGDSCLHKHANNAASVRAAESCIKSTVKIAKTMVSVDTSAAEL 472
 Db 421 PLDMSMGDSCLHKHANNAASVRAAESCIKSTVKIAKTMVSVDTSAAEL 472

RESULT 3
 Q4PLI4_HUMAN PRELIMINARY; PRT; 472 AA.
 ID Q4PLI4_HUMAN PRELIMINARY; PRT; 472 AA.
 AC Q4PLI4_HUMAN PRELIMINARY; PRT; 472 AA.
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DR Cannabinoid receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC	Homo sapiens (Human);
NCBI_TAXID=9606;	
RN	
RP	NUCLEOTIDE SEQUENCE.
[1]	RC TISSUE:Brain tumor;
RC	RA Kumar S.; Gupta S.; Shabana, Sharmina, Sharma G.; Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RL	CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR	DR -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR	EMBL: AF285025; AAF97250.1; - ; mRNA.
DR	GO; GO:0016021; C: integral to membrane; IEA.
DR	GO; GO:000949; P:cannabinoid receptor activity; IEA.
DR	GO; GO:0004872; F:receptor activity; IEA.
DR	GO; GO:0007186; G:G-protein coupled receptor activity; IEA.
DR	GO; GO:0007165; P:signal transduction; IEA.
DR	InterPro; IPR002230; Cnbind receptor.
DR	InterPro; IPR000810; Cnbind receptor.
DR	InterPro; IPR000810; Cnbind receptor.
DR	InterPro; IPR000276; GPCR_Rhodopsin.
DR	Pfam; PF00001; 7tm_1.1.
DR	Pfam; PF00022; CANNABINOID1R.
PRINTS	PRINTS; PRO00522; CANNABINOID1R.
PRINTS	PRINTS; PRO0362; CANNABINOID1R.
PRINTS	PRINTS; PRO0237; GPCR_RHODOPSIN.
PROSITE	PS00237; G: PROTEIN RECEP_F1_1; UNKNOWN_1.
DR	PROSITE; PS00237; G: PROTEIN RECEP_F1_1; UNKNOWN_1.
DR	PROSITE; PS5062; G: PROTEIN RECEP_F1_2; 1.
KW	G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SEQUENCE	SEQUENCE 472 AA; 52858 MW; 1D2E4@061D12ABP2 CRC64;
SQ	Query Match 99.5%; Score 2412; DB 2; Length 472; Best Local Similarity 99.6%; Pred. No. 2, 8e-156; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0; Query Match 99.5%; Score 2412; DB 2; Length 472; Best Local Similarity 99.6%; Pred. No. 2, 8e-156; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	1 MKSLDGLADTTFTITDLYLGNSNDIQYEDIKGDMSKLGYFPQKEPLTSFRGSFQE 60
Db	1 MKSLDGLADTTFTITDLYLGNSNDIQYEDIKGDMSKLGYFPQKEPLTSFRGSFQE 60
QY	61 KMTAGDNPOLVPADQVNITEFYKNSLSSFKENENIQGENENFIDIECTPMVNLPSQQLIA 120
Db	61 KMTAGDNPOLVPADQVNITEFYKNSLSSFKENENIQGENENFIDIECTPMVNLPSQQLIA 120
QY	121 VLSLTGIFTVLENLLVLCVILHSRSLRCPSTHFIGSLAVADLGSVTFYYSFIDPHVF 180
Db	121 VLSLTGIFTVLENLLVLCVILHSRSLRCPSTHFIGSLAVADLGSVTFYYSFIDPHVF 180
QY	181 HRKDSRNVLFLKGIGGTASFTASVGSLSLTTATARYISHRPLAYKRIVTRPKAVAFCLM 240
Db	181 HRKDSRNVLFLKGIGGTASFTASVGSLSLTTATARYISHRPLAYKRIVTRPKAVAFCLM 240
QY	241 WTAIVAVLPLGWCNECLOQSVDIIPHDIDETYLFWIGTISVLLFIVVAYMYILWK 300
Db	241 WTAIVAVLPLGWCNECLOQSVDIIPHDIDETYLFWIGTISVLLFIVVAYMYILWK 300
QY	301 AHSHAVRMHQRTQKSIIHTSEDGKVQTRDQARMIRAKTLVLLVLLICWGPILL 360
Db	301 AHSHAVRMHQRTQKSIIHTSEDGKVQTRDQARMIRAKTLVLLVLLICWGPILL 360
QY	361 AIMYYDVFGRMNKLKITVFAFCMSLCLNSTMVPIYALRSKDLRHAFRSMFPSCEGTQ 420
Db	361 AIMYYDVFGRMNKLKITVFAFCMSLCLNSTMVPIYALRSKDLRHAFRSMFPSCEGTQ 420
QY	421 PLDNMGDSDCLHKHANNAASVRAAESCIKSTVKIAKVTMSYSTDSAEAL 472
Db	421 PLDNMGDSDCLHKHANNAASVRAAESCIKSTVKIAKVTMSYSTDSAEAL 472
RESULT 4	RESULT 5
Q7LSP5 MACMU PRELIMINARY;	Q506J9_HUMAN PRELIMINARY;
Q7LSP5 MACMU PRELIMINARY;	ID Q506J9_HUMAN PRELIMINARY; PRTR; 472 AA.
AC Q506J9;	AC Q506J9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)	DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)	DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)	DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
Cannabinoid receptor CB-1.	Cannabinoid receptor type-1.
OS Macaca mulatta (Rhesus macaque).	OS Homo sapiens (Human).
OC Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
OC Cercopithecidae; Cercopithecinae; Macaca.	OC Homo.
NCBI_TAXID=9544;	NCBI_TAXID=9606;
[1]	[1]

QY	422 LDNSMGDSCLHGHANNAASVHRAESCIKSTVIKYAKVTMSVSTDTSSEAL 472	FT TOPO_DOM 144	155	Cytoplasmic (Potential).
Db	421 LDNSMGDSCLHGHANNAASVHRAESCIKSTVIKYAKVTMSVSTDTSSEAL 471	FT TRANSMEM 156	176	2 (Potential).
		FT TOPO_DOM 177	188	Extracellular (Potential).
		FT TRANSMEM 189	213	3 (Potential).
		FT TOPO_DOM 214	233	Cytoplasmic (Potential).
		FT TRANSMEM 234	256	4 (Potential).
		FT TOPO_DOM 257	274	Extracellular (Potential).
		FT TRANSMEM 275	300	5 (Potential).
		FT TOPO_DOM 301	345	Cytoplasmic (Potential).
		FT TRANSMEM 346	366	6 (Potential).
		FT TOPO_DOM 367	378	Extracellular (Potential).
		FT TRANSMEM 379	400	7 (Potential).
		FT TOPO_DOM 401	473	Cytoplasmic (Potential).
		FT CARBOHYD 78	78	N-linked (GlcNAc. . .) (Potential).
		FT CARBOHYD 84	84	N-linked (GlcNAc. . .) (Potential).
		SEQUENCE 473 AA;	52845 MW;	E59A6AFE17B646C CRC64;
		Query Match 96.7%; Score 2343.5; DB 1;	Length 473;	
		Best Local Similarity 96.8%; Pred. No. 1.3e-151;	5; Mismatches 9;	Indels 1; Gaps 1;
		Matches 458; Conservative 5;		
		Qy 1 MKSILDGLADTFRTRITDLYVGNDIQYEDIKGDAMSKLGYPPQKPLITSFRGSFQE 60		
		RC TISSUE=Brain Cortex;		
		RX MEDLINE=90332039; PubMed=2165569; DOI=10.1038/346561a0;		
		RA Matsuda L.A., Loait S.J., Brownstein M.J., Young A.C., Bonner T.I.;		
		RF "Structure of a cannabinoid receptor and functional expression of the cloned cDNA.",		
		RN Nature 346:561-564 (1990).		
		[2]		
		RP NUCLEOTIDE SEQUENCE.		
		RX MEDLINE=9642553; PubMed=8832654; DOI=10.1016/0304-3940(96)12792-0;		
		RA Ho B.Y., Zhao J.;		
		RR "Determination of the cannabinoid receptors in mouse x rat hybridoma NG108-15 cells and rat GH4Cl cells.",		
		RT J. Neurosci. Lett. 212:123-126 (1996).		
		[3]		
		RP NUCLEOTIDE SEQUENCE OF 1-107.		
		RX Shire D., Carillon C., Kaghad M., Calandra B., Rinaldi-Carmona M.,		
		RA Le Fur G., Caput D., Ferrara P.;		
		RR "An amino-terminal variant of the central cannabinoid receptor resulting from alternative splicing.",		
		RL J. Biol. Chem. 270:3726-3731 (1995).		
		CC -I- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by CC inhibiting adenylyl cyclase. Could be a receptor for anandamide.		
		-I- SUBCELLULAR LOCATION: Integral membrane protein.		
		-I- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.		
		CC This Swiss-Prot entry is copyright. It is produced through a collaboration CC between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use as long as its content is in no way modified and this statement is not removed.		
CC	DR EMBL; X55812; CAA39332.1; -; mRNA.	RESULT 8		
	DR EMBL; U40395; AA39067.1; -; mRNA.	CNR1 MOUSE STANDARD;		
	DR PIR; A33117; A33117.	ID CNR1 MOUSE		
	DR Ensembl; ENSEMBL0000008223; Rattus norvegicus.	AC P47766,		
	DR RGD; 2359; Chrl.	DT 01-FEB-1996 (Rel. 33, Created)		
	DR InterPro; IPR002230; Cnbind receptor.	DT 01-FEB-1996 (Rel. 33, Last sequence update)		
	DR InterPro; IPR00810; Cnbind receptor1.	DT 10-MAY-2005 (Rel. 47, Last annotation update)		
	DR InterPro; IPR000216; GPCR_Rhodopsin.	DB Cannabinoid receptor 1 (CBL) (CB-R) (Brain-type cannabinoid receptor).		
	DR PANTHER; PTHR19256; SF8; Cnbind_receptor1; 1.	GN Name=Char1;		
	DR Pfam; PF0001; 7em_1; 1.	OS Mus musculus (Mouse).		
	DR PRINTS; PR00522; CANNABINOIDR.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	DR PRINTS; PR00362; GPCR_RHODOPSN.	OC Mammalia; Buteraria; Euarchontoglires; Glires; Rodentia; Sciurognathi;		
	DR PROSITE; PS00237; G_protein_RECEP_F1.1; 1.	OC Muridae; Murinae; Mus.		
	DR PROSITE; PS50262; G_protein_RECEP_F1.2; 1.	OX NCBI_TaxID=10909;		
	KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;	RN [1] NUCLEOTIDE SEQUENCE.		
	KW Transmembrane.	RC STRAIN=C57BL/6; TISSUE=Brain;		
	FT TOPO_DOM 1 117	RC MEDLINE=96272305; PubMed=877318;		
	FT TRANSMEM 1 143	RX RA Chakrabarti A., Onalvi E.S., Chaudhuri G.;		

"Cloning and sequencing of a cDNA encoding the mouse brain-type cannabinoid receptor protein."; DR Ensembl; ENSMUSG0000044288; Mus musculus.

RT MG1; MGI:10415; Cntr. DR GO:GO:0016031; C:internal to membrane; TAS.

RL [2] DR InterPro; IPRE002230; Chnoid receptor.

RN DR InterPro; IPRE000810; Chnoid receptor1.

RC DR InterPro; IPRE000276; GPCR Rhodopsin.

STRAIN=129; DR PANTHER; PTIHE19266-SF8; Chnoid receptor1; 1.

RA Bonner T.I.; DR Pfam; PF00001; 7cm; 1.

RA Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases. DR PRNTS; PR00522; CANNABINOIDR.

[3] DR PRINTS; PR00562; CANNABINOIDR.

RP NUCLEOTIDE SEQUENCE. DR PRINTS; PR00537; GPCR Rhodopsin.

RX MEDLINE=9624953; PubMed=8832654; DOI=10.1016/0304-3940(96)12792-0; DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.

RA Ho B.Y.; Zhao J.; DR PROSITE; PS00262; G PROTEIN RECEPTOR_F1_2; 1.

RT "Determination of the cannabinoid receptors in mouse x rat hybridoma NG108-15 cells and rat GH4C1 cells."; DR G-protein coupled receptor; Glycoprotein; Receptor; Transducer; KW Transmembrane.

RL Neurosci. Lett. 212:123-126(1996). DR TOPO_DOM 1 117

RN [4] DR TRANSMEM 1 143

RP NUCLEOTIDE SEQUENCE. DR TOPO_DOM 1 144

RC STRAIN=129/Sv; DR TRANSMEM 1 155

RX MEDLINE=98105909; PubMed=9888857; DOI=10.1126/science.283.5400.401; DR TRANSMEM 1 176

RA Leident C.; Valverde O.; Cosbu G.; Petitet F.; Aubert J.P.; Beslot F.; DR TRANSMEM 1 188

RA Boehme G.A.; Imperato A.; Pedrazzini T.; Roques B.P.; Vassart G.; DR TRANSMEM 1 213

RA Pratta W.; Parmentier M.; DR TOPO_DOM 1 214

RT "Unresponsiveness to cannabinoids and reduced addictive effects of opiates in CBL receptor knockout mice."; DR TRANSMEM 1 233

RL Science 283:401-404(1999). DR TOPO_DOM 1 234

[5] DR TRANSMEM 1 256

RP NUCLEOTIDE SEQUENCE. DR TOPO_DOM 1 257

RC STRAIN=C5BL/6; TISSUE=Brain; DR TRANSMEM 1 274

RX MEDLINE=22388277; PubMed=12477932; DOI=10.1073/pnas.242603899; DR TRANSMEM 1 300

RA Strausberg R.L.; Feingold B.A.; Grouse L.H.; Derge J.G.; DR TRANSMEM 1 301

RA Klausner R.D.; Collins F.S.; Wagner L.; Shemesh C.M.; Schuler G.D.; DR TRANSMEM 1 345

RA Hopkins R.P.; Jordan H.; Moore T.; Moore T.; Max S.I.; Wang J.; Hsieh F.; DR TRANSMEM 1 367

RA Diatchenko L.; Marusina K.; Farmer A.A.; Rubin G.M.; Hong L.; DR TRANSMEM 1 379

RA Stapleton M.; Soares M.B.; Bonaldo M.F.; Casavant T.L.; Scheetz T.E.; DR TRANSMEM 1 400

RA Brownstein M.J.; Usdin T.B.; Toshiyuki S.; Carninci P.; Prange C.; DR TRANSMEM 1 473

RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.; DR TRANSMEM 1 78

RA Roskars S.A.; McIwan P.J.; McKernan K.J.; Malek J.A.; Gunnaraine P.H.; DR CARBOHYD 1 84

RA Richards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay J.J.; Hulyk S.W.; DR CONFLICT 1 9

RA Villalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.; DR CONFLICT 1 9

RA Fahey J.; Helton E.; Ketteman M.; Madan A.; Rodrigues S.; Sanchez A.; DR CONFLICT 1 115

RA Whiting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.; DR CONFLICT 1 211

RA Blakesley R.W.; Touchman J.W.; Green B.D.; Dickson M.C.; DR CONFLICT 1 211

RA Rodriguez A.C.; Grinblat Y.S.N.; Krzywinski M.I.; Skalska U.; Smailius D.E.; DR CONFLICT 1 211

RA Butcher D.K.; Schein J.B.; Jones S.J.M.; Marra M.A.; DR CONFLICT 1 211

RA Schniech A.; Schein J.B.; Jones S.J.M.; Marra M.A.; DR CONFLICT 1 211

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; DR CONFLICT 1 211

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002). DR CONFLICT 1 211

CC -!- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by inhibiting adenylylate cyclase. Could be a receptor for anandamide. DR CONFLICT 1 211

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. DR CONFLICT 1 211

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family. DR CONFLICT 1 211

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CC DR EMBL; U17985; AA57202.1; -; mRNA.

CC DR EMBL; U42968; AA64413.1; -; Genomic_DNA.

CC DR EMBL; U40709; AA91176.1; -; mRNA.

CC DR EMBL; AF153345; AAD3624.1; -; mRNA.

CC DR EMBL; Y18374; CB42641.1; -; Genomic_DNA.

CC DR EMBL; BC070447; AAH70447.1; -; mRNA.

CC DR EMBL; BC079564; AAH79564.1; -; mRNA.

RESULT 9
 Q5SF33_MOUSE, MOUSE PRELIMINARY; PRT; 473 AA.
 ID Q5SF33;
 AC ;
 DT 01-FEB-2005 (TREMBLref. 29; Created)
 DT 01-FEB-2005 (TREMBLref. 29; Last annotation update)
 DT 10-MAY-2005 (TREMBLref. 30; Last annotation update)
 DE Striatal cannabinoid receptor type 1 protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B6CBA;
 RX PubMed:15606779; DOI:10.1111/j.1432-1033.2004.04460.x;
 RA McCaw E.A., Hu H., Gomez G.T., Hebb A.L., Kelly M.E.,
 RA Denovan-Wright E.M.;
 RA "Structure, expression, and regulation of the cannabinoid receptor gene
 (cB1) in Huntington's disease transgenic mice.",
 RL Eur. J. Biochem. 271:909-920(2004).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- SIMILARITY: Belongs to the G-Protein coupled receptor 1 family.
 DR EMBL: AY522555; AAS91801.1; -; Genomic_DNA.
 DR EMBL: AY522554; AAS91800.1; -; mRNA.
 DR MGII; MGII:104515; Chr1.
 DR GO:00016021; C:integral to membrane; TAS.
 DR InterPro; IPR002320; Cnoid_receptor.
 DR InterPro; IPR000810; Cnoid_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7cm 1; 1.
 DR PRINTS; PR00522; CANABINOID1R.
 DR PRINTS; PR00362; CANNABINOIDR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
 DR PROSITE; PS50262; G-PROTEIN RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transducer; Transmembrane.
 KW Sequence 473 AA; 52831 MW; B50418191cb6429 CRC64;
 SQ

Query Match 1
 Best Local Similarity 96.6%; Score 2340.5; DB 2; Length 473;
 Matches 457; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MKSTLDGLADTTFTITDLYGSNDIQYEDIKGDMASKLGYPQQPLTSFRGSPQQE 60
 Db 1 MKTAGDNPOLVPA-DQVNTIEFYNKSLSKFKEENIDGENTMIEFVNIPNSQQLAI 119
 Db 61 KMTAGDNPOLVPA-DQVNTIEFYNKSLSKFKEENIDGENTMIEFVNIPNSQQLAI 120
 Db 61 KMTAGDNPOLVPA-DQVNTIEFYNKSLSKFKEENIDGENTMIEFVNIPNSQQLAI 120
 Db 120 AVLSLTIGFTVLENLIVLVLHSRSLRCPSPHYTIGSSLAVADLSSVITYFSFDTHV 179
 Qy 121 AVLSLTIGFTVLENLIVLHSRSLRCPSPHYTIGSSLAVADLSSVITYFSFDTHV 180
 Db 180 FHRKDSRVNLFKUGGVATPSATGSEFLTARYISIHRPLAYKRIVTRPKAVAFCL 239
 Qy 181 FHRKDSRVNLFKUGGVATPSATGSEFLTARYISIHRPLAYKRIVTRPKAVAFCL 240
 Db 240 MWTAIAVAVLPLIGWNCVKLQSYCSDFPHIDTYLFWIGTVSILLFIVYAYMLW 299
 Db 241 MWTAIAVAVLPLIGWNCVKLQSYCSDFPLIDTYLFWIGTVSILLFIVYAYMLW 300
 Qy 300 KAHSHAVMTOGTOKSIIHTSEDGKVTCYTRPKQARWAIRAKTLVILVYLICMPL 359
 Db 301 KAHSHAVMTOGTOKSIIHTSEDGKVTCYTRPKQARWAIRAKTLVILVYLICMPL 360
 Qy 360 LAINMYDVGKMKLKLKITYFAFCSMCLCINSTNPYIYALRSKDLRFAFRSMPPSCSGTA 419
 Db 361 LAINMYDVGKMKLKLKITYFAFCSMCLCINSTNPYIYALRSKDLRFAFRSMPPSCSGTA 420

Qy 420 QPLDNNSMGDSCLHKHANNAASVHRAESCIKSTVKIAKVTMSVSTDTSAAEL 472
 Db 421 QPLDNNSMGDSCLHKHANNTASMHRAESCIKSTVKIAKVTMSVSTDTSAAEL 473
 RESULT 10
 CNRI_FELCA STANDARD; PRT; 472 AA.
 ID CNRI_FELCA
 AC 002777;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DB Cannabinoid receptor 1 (cB1) (CB-R).
 Name=CNR1;
 OS Felis silvestris catus (Cat)
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
 OC Felinae; Felis.
 OX NCBI_TAXID=9685;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gebremedhin D., Lange A.R., Ably M.R., Campbell W.B., Hillard C.J., Harder D.R.; RT "The cannabinoid CB1 receptor is expressed in cat cerebral arterial muscle cells and functions to inhibit L-type Ca2+ channel current.";
 RL Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
 CC -!- FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by inhibiting adenylyl cyclase. Could be a receptor for anandamide.
 CC Inhibits L-type Ca (2+) channel current.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed in cerebral arterial muscle cells.
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC EMBL; U94342; AAB53440.1; -; mRNA.
 DR InterPro; IPR00230; Cnoid receptor.
 DR InterPro; IPR000810; Cnoid receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR PANTHER; PT00001; 7cm 1; 1.
 DR PRINTS; PR00522; CANNABINOID1R.
 DR PRINTS; PR00362; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1; 1.
 DR PROSITE; PS00262; G-PROTEIN RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer;
 KW Transmembrane.
 FT TOPO_DOM 1 116 Extracellular (Potential).
 FT TRANSMEM 117 142 1 (Potential).
 FT TOPO_DOM 143 154 Cytoplasmic (Potential).
 FT TRANSMEM 155 175 2 (Potential).
 FT TOPO_DOM 176 187 Extracellular (Potential).
 FT TRANSMEM 188 212 3 (Potential).
 FT TOPO_DOM 213 232 Cytoplasmic (Potential).
 FT TRANSMEM 233 255 4 (Potential).
 FT TOPO_DOM 256 273 Extracellular (Potential).
 FT TRANSMEM 274 299 5 (Potential).
 FT TOPO_DOM 300 344 Cytoplasmic (Potential).
 FT TRANSMEM 345 365 6 (Potential).
 FT TOPO_DOM 366 377 Extracellular (Potential).
 FT TRANSMEM 378 399 7 (Potential).
 FT TOPO_DOM 400 472 Cytoplasmic (Potential).
 FT CARBOHYD 77 77 N-linked (GlcNAc . .) (Potential).
 FT CARBOHYD 83 83 N-linked (GlcNAc . .) (Potential).
 SQ SEQUENCE 472 AA; 52887 MW; A2774DBFB8P2DAF34 CRC64;
 Query Match 96.3%; Score 2335; DB 1; Length 472;

Best Local Similarity 95.8%; Pred. No. 5e-151; 7; Indels 0; Gaps 0;

Matches 452; Conservative 13; Mismatches 7; DR PRINTS; PRO0522; CANNABINOIDR.

DR PRINTS; PR00562; CANNABINOIDR.

DR PRINTS; PR00237; GPROTEIN-RECSBP_F1_1; 1.

DR PROSITE; PS00337; G-PROTEIN-RECSBP_F1_1; 1.

DR PROSITE; PS52622; G-PROTEIN-RECEBP_F1_1; 1.

KW G-protein coupled receptor; Glycoprotein; Receptor; Transducer; Transmembrane; KW Transmembrane; 118

FT TOPO_DOM 1

FT TRANSMEM 119

FT TRANSMEM 144

FT TOPO_DOM 145

FT TRANSMEM 156

FT TRANSMEM 157

FT TOPO_DOM 177

FT TRANSMEM 178

FT TRANSMEM 189

FT TRANSMEM 190

FT TOPO_DOM 214

FT TRANSMEM 215

FT TRANSMEM 234

FT TRANSMEM 235

FT TOPO_DOM 257

FT TRANSMEM 258

FT TRANSMEM 275

FT TRANSMEM 301

FT TOPO_DOM 302

FT TRANSMEM 346

FT TRANSMEM 347

FT TOPO_DOM 368

FT TRANSMEM 379

FT TRANSMEM 380

FT TOPO_DOM 401

FT TRANSMEM 402

FT CARBOHYD 79

FT CARBOHYD 79

SQ SEQUENCEC 473 AA; 53094 MW; 98EC61BD22461E CRC65;

Query Match 92.8%; Score 2250.5; DB 1; Length 473;

Best Local Similarity 91.4%; Pred. No. 2.9e-145;

Matches 433; Conservative 25; Mismatches 13; Indels 3; Gaps 2;

Db 1 MKSLIDGLADTPRTITDLYVGSNDIQCYEDDIKGDMASKLGYPPQKFPLTSFRGSPFQE 60

Db 1 MKSLIDGLADTPRTITDLYVGSNDIQCYEDDMKGDMASKLGYEQKFPLTSFRGSPFQE 60

Qy 1 RMTAGDNP--OLVIAQDNITEFNKSLSFFKENBENIQCGENFDIECPMVLNPSQQLA 118

Db 1 KMTGGDDSLSLISIIPSEQVNITEFNKSLSLTFKDNNEENIQCGENFDMECPMVLNPSQQLA 120

Qy 119 IAVLSLTGTFETVNLVCLVILHRSRLCRPSYHFIGSLAVADLGSIYSPIDEYVF 178

Db 121 IAVLSLTGTFETVNLVCLVILHRSRLCRPSYHFIGSLAVADLGSIYSPIDEYVF 180

Qy 179 VFHRKDSRATVFLFKLGYYTASFTASYGSPLTATARYISIHRPLAYKRIVTRPKAVVAFC 238

Db 181 VFHRKDSRATVFLFKLGYYTASFTASYGSPLTATARDYISIHRPLAYKRIVTRPKAVVAFC 240

Qy 239 LMWTIAIVIAVPLIGWNCNLKQSTVKAUTMSVSTDTSAAEL 298

Db 301 WKAHSHAVRMIQRGTOKSIIHTSSEDGKVQVTRPQARMIRLAKTLLVLUVLIICWGP 358

Qy 359 LLAIAMYYDFEGKMKLKLITYFAFCSMLCLNISTNPVIALRSKDLRHAFRSMFPSCEGT 418

Db 361 LLAIAMYYDFEGKMKLKLITYFAFCSMLCLNISTNPVIALRSKDLRHAFRSMFPSCEGT 420

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CC -----

CC EMBL; AF253388; AAFT7049_1; -; mRNA.

RA Soderstrom K.; Johnson F.;

RT Behavioral, pharmacological and molecular characterization of a zebra finch CB1 cannabinoid receptor.";

RL Submitted (APR-2000) to the ENSEMBL/GenBank/DBJ databases.

CC - FUNCTION: Involved in cannabinoid-induced CNS effects. Acts by inhibiting adenylylate cyclase (by similarity).

CC - SUBCELLULAR LOCATION: Integral membrane protein.

CC - SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

CC -----

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CC -----

DR EMBL; AF253388; AAFT7049_1; -; mRNA.

DR InterPro; IPR00230; Chbnd receptor.

DR InterPro; IPR00810; Cnoid receptor.

DR InterPro; IPR00276; GPCR_RhoGDP.

DR PANTHER; PTM1966; SP8; Chbnd_receptor1; 1.

DR Pfam; PF00001; 7tm_1; 1.

RESULT 12

QSUB37_HUMAN PRELIMINARY; PRT; 439 AA.

ID QSUB37_HUMAN PRELIMINARY; PRT; 439 AA.

AC QSUB37_HUMAN PRELIMINARY; PRT; 439 AA.

DT 01-FEB-2005 (TREMBLrel. 29, Created)

DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)

DB Cannabinoid receptor 1 splice variant CB1b.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
Homo.
NCBI_TAXID=9606;
OX [1]
RN NUCLEOTIDE_SEQUENCE.
RP PubMed=15620723; DOI=10.1016/j.febslet.2004.11.085;
RX Ryberg B., Vu H.K., Larsson N., Groblewski T., Hjorth S., Elebring T.,
RA Stjøren S., Greasley P.J.;
RA "Identification and characterisation of a novel splice variant of the
human CB1 receptor";
RR FEBS Lett. 579:255-264 (2005).
RL [2]
RN NUCLEOTIDE_SEQUENCE.
RA Khang Vu H., Groblewski T., Greasley P.;
RL Submitted (SPP=2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR_LOCATION: Integral membrane protein (By similarity).
-1- SIMILARITY: Belongs to the G-protein coupled receptor_1 family.
DR EMBL; AY766182; AAU35030.1; -; mRNA.
GO; GO:0016021; C-integral to membrane; IFA.
DR GO; GO:004949; F-cannabinoid receptor activity; IEA.
DR GO; GO:0004872; P-receptor activity; IEA.
DR GO; GO:0007186; P-G-protein coupled receptor protein signalin. . ; IEA.
DR InterPro; IPR002210; G-protein coupled receptor; IEA.
DR InterPro; IPR000810; Cnbind receptor.
DR InterPro; IPR00216; GPCR_Rhodopsin.
DR PRINTS; PR00522; CANNABINOIDR.
DR PRINTS; PR00362; CANNABINOIDR.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G-PROTEIN RECEP_F1_1.
DR PROSITE; PS50462; G-PROTEIN RECEP_F1_1.
KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 439 AA; C80C6BBD640412C1 CRC64;

Query Match 91.2%; Score 209.5; DB 2; Length 439;
Best Local Similarity 92.6%; Pred. No. 1.7e-142;
Matches 437; Conservative 0; Mismatches 2; Indels 33; Gaps 1;

Qy 1 MKSTILDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Db 1 MKSTILDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Qy 1 MKSTILDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Db 1 MKSTILDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Qy 61 KMTAGDNIPOLYPADQVNITEPYKNSLSKPKENENIQGENFMIECTMVLNPSQQLIA 120
Db 28 KMTAGDNIPOLYPADQVNITEPYKNSLSKPKENENIQGENFMIECTMVLNPSQQLIA 87
Qy 121 VLSLTLLGTFTVLENLVLVCLTILRSLSLRCPSTHFIGSLAVDLIGSTIIVTFSIDFVVF 180
Db 88 VLSLTLLGTFTVLENLVLVCLTILRSLSLRCPSTHFIGSLAVDLIGSTIIVTFSIDFVVF 147
Qy 181 HRKDSRNVTFPLKLGSGVTAFTASVGSLFLTATAIRYITHRPLAYKTRVTRPKAVAFCLM 240
Db 148 HRKDSRNVTFPLKLGSGVTAFTASVGSLFLTATAIRYITHRPLAYKTRVTRPKAVAFCLM 207
Qy 241 WTIATIVIAVLPLIGWNCLEQSVSDIPPHIDETYLMTGIGTSVSLFLIVAYMYILINK 300
Db 208 WTIATIVIAVLPLIGWNCLEQSVSDIPPHIDETYLMTGIGTSVSLFLIVAYMYILINK 267
Qy 301 AHSHAVRMHQRTGOKTSIITHTSEGDQVTRPDAIRALAKTLVLLVLLICWGLL 360
Db 268 AHSHAVRMHQRTGOKTSIITHTSEDGKVQTRPDAIRALAKTLVLLVLLICWGLL 327
Qy 361 AIMYYDVFGRQNKLIKTVFAFCSMILCLNSTNPVIIYALRSKDLRHSRSMFPSCEGTQ 420
Db 328 AIMYYDVFGRQNKLIKTVFAFCSMILCLNSTNPVIIYALRSKDLRHSRSMFPSCEGTQ 387
Qy 421 PLDNMGPSDCLKHANNAASVHAAECSIKSTVKIAKVTMSVSTDTSAEAL 472
Db 388 PLDNMGPSDCLKHANNAASVHAAECSIKSTVKIAKVTMSVSTDTSAEAL 439

Query Match 85.2%; Score 2064.5; DB 1; Length 473;
Best Local Similarity 83.5%; Pred. No. 1.e-132;
Matches 396; Conservative 39; Mismatches 36; Indels 3; Gaps 2;

Qy 1 MKSLDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Db 1 MKSLDGLADTTFRITITDLYVGSNDIQYEDIKGDMASKLGYPQQKPLTSFRGSPFQ 60
Qy 61 KMTAGDNIPOLYVADQYNTFKNSLSKPKENENIQGENFMIECTMVLNPSQQLIA 118
Db 61 KMTAGDNIPOLYVADQYNTFKNSLSKPKENENIQGENFMIECTMVLNPSQQLIA 120

RESULT 14

Q801IM1_XENLA	NUCLEOTIDE SEQUENCE;	PRT;	470 AA.
Q801IM1	XENLA PRELIMINARY;		
AC			
DT	01-JUN-2003 (TREMBLrel. 24, Created)		
DT	01-OCT-2003 (TREMBLrel. 24, Last annotation update)		
DB	CBD cannabinoid receptor.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodidae; Xenopus; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RR	MEDLINE=22234076; PubMed=112297261; DOI=10.1016/S0891-0618(02)00040-6;		
RA	Salio C., Cottone B., Conrath M., Franzoni M. F. ¹		
RT	"CBD cannabinoid receptors in amphibian spinal cord: relationships with some nociception markers." J. Chem. Neuroanat. 24:153-162 (2002).		
RL	[2]		
RN	NUCLEOTIDE SEQUENCE.		
RR	MEDLINE=22782291; PubMed=12909919; DOI=10.1002/cne.10808;		
RA	Cottone B., Salio C., Conrath M., Franzoni M. F. ¹		
RT	"Xenopus laevis CBD cannabinoid receptor: molecular cloning and mRNA distribution in the central nervous system." J. Comp. Neurol. 464:487-496 (2003).		
RN	[3]		
RP	NUCLEOTIDE SEQUENCE.		
RA	Cottone E. ¹		
RL	Submitted (APP-2002) to the EMBL/GenBank/DBJ databases.		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).		
EMBL	AY098532; AAM26314.1; -; mRNA.		
DR	GO; GO:0016021; C: integral to membrane; IEA.		
DR	GO; GO:0004949; F:cannabinoid receptor activity; IEA.		
DR	GO; GO:0004872; F:receptor activity; IEA.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.		
DR	GO; GO:0007165; P:signal transduction; IEA.		
DR	InterPro; IPR002230; Cnbind receptor.		
DR	InterPro; IPR000810; Cnoid receptor.		
DR	InterPro; IPR000276; GPCR_Rhodopsin.		
DR	Pfam; PF00001; 7cm_1, 1.		
DR	PRINTS; PR00522; CANNABINOID1R.		
DR	PRINTS; PR00362; CANNABINOIDR.		
DR	PRINTS; PR00237; GPCRRODPSN.		
DR	PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.		
DR	PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.		

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.

SQ	G-PROTEIN COUPLED RECEPTOR; RECEPTOR; TRANSDUCER; TRANSMEMBRANE.		
Query	119 IAVLSLTGLSTFTVLENLYCIVLHSRSIRCRPSYHFIGSLAVADLLGSVIFVYSFIDFH 178	Match	83.8%; Score: 2031; DB 2; Length: 470;
Db	121 IAVLSLTGLSTFTVLENFLVCLQLSQTURCRPSTHISLAVADLLGSVIFVTSFLDH 180	Best Local Similarity	82.7%; Pred. No. 2.7e-130;
Query	179 VPERKDSRNVPFLPKLGGTASFTASVGSSLFTALARISITHRPLAYKRIVTRPKAVAFC 238	Matches	391; Conservative: 43; Mismatches: 35; Indels: 4;
Db	181 VPERKDSRNVPFLPKLGGTASFTASVGSSLFTALARISITHRPLAYKRIVTRPKAVAFC 240	Qy	1 MKSLIDGLADTTPTTTITDLYVGSNDIQEYDIKGDMASKLGYPPQKEPLTSFRCSPFQB 60
Query	239 LMWTIAITIAVLPLGNCEKLQSYCSDIPHIDETYLAFWIGTSVLLFIVYAYMXT 298	Db	1 MKSLIDGLADTTPTTTITDLYVGSNDIQEYDDSSKGDISSKLVYPPQKLPLSSLRDPDHLH 60
Db	241 LMWTIAITIAVLPLGNCEKLQSYCSDIPHIDETYLAFWIGTSVLLFIVYAYVYT 300	Qy	61 KMTAGDNPOL-VPAQDNVNTEFYNSLSSPKENENBIOGENFMIDIECPMVNLNSQOLAI 119
Query	299 WKAHSHAVRMVQRTGQSKIIHTSEDGKVQTRPQAHAIRLAKTLVILWVLIQNCSP 358	Db	61 KMTIDDDPLSIPDQINATDPYNSKSI-1FKDTDNNVQCGKFNDFMECMFLTSQSQLVVI 119
Db	301 WKASHAVRMVQRTGQSKIIHTSEDGKVQTRPQAHIRLAKTLVILWVLIQNCSP 360	Qy	120 AVLSUTLGLFTYLNLLVLCVILSRSLCRPSYHFIGSLAVADLLGSVIFVTSVDFHV 179
Query	359 LLAINMVYDVFQKMNLKIKTVYAFCSMLCLINSTVNPIITYALRSIDLRAFRSMFSPSCEGT 418	Db	120 AALSLTIGLTTVLMMLVLLVIVSRSLRCPSYHFIGSLAVADLLGSVIFVTSVDFHV 179
Db	361 LLAINMVYDVFQKMNLKIKTVYAFCSMLCLMDSTVNPIITYALRSIDLRAFLEQCPCEGT 420	Qy	180 PHRQDSRNVPFLKGQGGVTAFTASVGSLSLTALARISITHRPLAYKRIVTRPKAVAFCL 239
Query	419 AQPLONSMGSDCLKHANNAASVERAACIJKSTVKIAKVTMSYSTDSABAL 472	Db	180 FHRQDSRNVPFLKGQGGVTAFTASVGSLSLTALARISITHRPMYSYKTRIVTRPKAVAFCL 239
Db	421 SQPLDNM-ESDQCRRHGNAGNAGVHAAENCIKSTVKIAKVTMSYSTETSGEAV 473	Qy	240 MWTAIVIAVIALPLGWNCBKQSDFPHIDESTLMWIGTYSVLLPVIVYAMYILW 299
Db		Db	240 MWTAIVIAVIALPLGWNCIKLRSVCSDFPLDIDTYLMWIGTYSVLLPVIVYAMYILW 299
Qy		Qy	300 KAHHFAVRM1QRTGQSKIIHTSSEPGKVQTRPQDAIRLAKTLVILWVLIICGPL 359
Db		Db	300 KAHHFAVRM1QRTGQSKIIVHTSEPGKVHTPQDAIRLAKTLVILWVLIICGPL 359
Qy		Qy	360 LAIMMYDVFQKMNLKIKTVYAFCSMLCLINSTVNPIITYALRSIDLRAFRSMFSPSCEGTA 419
Db		Db	360 MAIMYYDVFQKMNLKIKTVYAFCSMLCLINSTVNPIITYALRSIDLRAFCMSPSCQGTA 419
Qy		Qy	420 QPLDNMGSDDCLKHANNAASVERAACIJKSTVKIAKVTMSYSTDSABAL 472
Db		Db	420 QPLDNMGSDDCLKHANNAASVERAACIJKSTVKIAKVTMSYSTDSABAL 472
Qy		Qy	420 QPLDNM-ESDQCRRHGNAGNAGVHAAENCIKSTVKIAKVTMSYSTDSABAL 472
Db		Db	420 QPLDNM-ESDQCRRHGNAGNAGVHAAENCIKSTVKIAKVTMSYSTDSABAL 472
RN	[1]	RN	NCBI_TaxID=9606;
RP	NUCLEOTIDE SEQUENCE.	RP	NCBI_TaxID=9606;
RA	Salio C., Cottone B., Conrath M., Franzoni M. F. ¹	RA	Williams S./
RT	"CBD cannabinoid receptors in amphibian spinal cord: relationships with some nociception markers." J. Chem. Neuroanat. 24:153-162 (2002).	RT	Submitted (MAY-2005) to the ENBL/GenBank/DBJ databases.
RL	[2]	RL	-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
RN		CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
RR		CC	EMBL: AL136096; CAI19916.1; -; Genomic DNA.
DR		DR	DR GO; GO:001621; C:integral to membrane; IEA.
DR		DR	DR GO; GO:0004949; F:cannabinoid receptor activity; IEA.
DR		DR	DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; IEA.
DR		DR	DR InterPro; IPR002230; Cnbind receptor.
DR		DR	DR InterPro; IPR000810; Cnoid receptor.
DR		DR	DR InterPro; IPR000276; GPCR_Rhodopsin.
DR		DR	DR Pfam; PF00001; 7cm_1, 1.
DR		DR	DR PRINTS; PR00522; CANNABINOID1R.
DR		DR	DR PRINTS; PR00362; CANNABINOIDR.
DR		DR	DR PRINTS; PR00237; GPCRRODPSN.
DR		DR	DR PROSITE; PS00237; G PROTEIN RECEP_F1_1; UNKNOWN_1.
DR		DR	DR PROSITE; PS50262; G PROTEIN RECEP_F1_2; 1.

KW G-protein coupled receptor; Receptor; Transducer; Transmembrane.
SQ SEQUENCE 411 AA; 45874 MW; B3C31AcAB4066BC1 CRC4;

Query Match	80.6%	Score 1954;	DB 2;	Length 411;
Best Local Similarity	98.5%	Pred. No. 4.1e-125;		
Matches	382;	Conservative	1;	Mismatches 5;
				Indels 0;
				Gaps 0;

Qy 85 SLSSEPKENPENIQCGENFMIDECPMVNLPSQQLAIAVISLTLGTFVLENLLVLCVILHS 144
Db 24 STKTSKENEENIQCGENFMIDECPMVNLPSQQLAIAVISLTLGTFVLENLLVLCVILHS 144
Qy 145 RSLRCRSPYTHFIGSLAVADLLGSVIFYFSFIDPFVFKDSRNVFLPLGGTTASFTPSV 204
Db 84 RSLRCRSPYTHFIGSLAVADLLGSVIFYFSFIDPFVFKDSRNVFLPLGGTTASFTPSV 143
Qy 205 GSLPLTALARYIStHRLPLAYKRIVTRPKAVVAFCLMWTTIAIVTAVLPFLGNCCEKLO SVC 264
Db 144 GSLFLTALDRYIStHRLPLAYKRIVTRPKAVVAFCLMWTTIAIVTAVLPFLGNCCEKLO SVC 203
Qy 265 SDIFPHIDDTYLMFWIGTISVLLPIVAYAMYIILWKASHAVRMIQRTQKSIIHTSED 324
Db 204 SDIFPHIDDTYLMFWIGTISVLLPIVAYAMYIILWKASHAVRMIQRTQKSIIHTSED 324
Qy 325 GKIVYTRPQDQARMAIRLAKTLVLLVLLICMGPLLAIMYDVFGKMKLIKIVFAFCSM 384
Db 264 GKIVYTRPQDQARMDIRLAKTLVLLVLLICMGPLLAINYDVFGKMKLIKIVFAFCSM 323
Qy 385 LCLLNSTNPITIYLRSKDLRHAFRSMPSCEGTAOPLDNSMGDSDCIHCKHANNAASVHR 444
Db 324 LCLLNSTNPITIYLRSKDLRHAFRSMPSCEGTAOPLDNSMGDSDCIHCKHANNAASVHR 383
Qy 445 AAESCIKSTVKAKVTMVSYSTDSEAEL 472
Db 384 AAESCIKSTVKAKVTMVSYSTDSEAEL 411

Search completed: January 6, 2006, 21:12:26
Job time : 235 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	2424	100.0	472	5	US-10-521-420-1	Sequence 1, App1
2	2412	99.5	472	4	US-10-525-57A-84	Sequence 84, App1
3	2412	99.5	472	4	US-10-536-33685	Sequence 33685, App1
4	2412	99.5	472	4	US-10-295-07-236	Sequence 236, App1
5	2412	99.5	472	4	US-10-764-45-168	Sequence 168, App1
6	2412	99.5	472	5	US-10-482-039-172	Sequence 172, App1
7	2412	99.5	472	6	US-11-019-829-88	Sequence 88, App1
8	2407	99.3	472	3	US-09-926-509-469	Sequence 469, App1
9	2407	99.3	472	5	US-10-935-05-469	Sequence 469, App1
10	2401	99.1	472	4	US-10-295-027-238	Sequence 238, App1
11	1954	80.6	411	4	US-10-295-037-240	Sequence 240, App1
12	1954	80.6	411	4	US-10-408-765A-2310	Sequence 2310, App1
13	1954	80.6	411	6	US-11-019-829-89	Sequence 89, App1
14	710	29.3	360	4	US-10-225-567A-86	Sequence 86, App1
15	710	29.3	360	4	US-10-590-078-3	Sequence 3, App1
16	710	29.3	360	5	US-10-473-127-1541	Sequence 1541, App1
17	710	29.3	360	5	US-10-473-127-1541	Sequence 1542, App1
18	710	29.3	360	5	US-10-473-127-1543	Sequence 1543, App1
19	710	29.3	360	5	US-10-473-127-1544	Sequence 1544, App1
20	705	29.1	360	3	US-09-926-509-471	Sequence 471, App1
21	705	29.1	360	5	US-10-935-05-471	Sequence 471, App1
22	410	16.9	80	3	US-09-933-844-50	Sequence 36, App1
23	410	16.9	80	4	US-10-633-438-36	Sequence 38, App1
24	410	16.9	80	5	US-10-633-164-38	Sequence 36, App1
25	410	16.9	80	5	US-10-901-772-36	Sequence 50, App1
26	410	16.9	80	6	US-11-036-435-50	Sequence 8, App1
27	369.5	15.2	364	4	US-10-764-425-330	Sequence 489, App1

ALIGNMENTS

RESULT 1
US-10-521-420-1
; Sequence 1, Application US/10521420
; Publication No. US2005023133A1
; GENERAL INFORMATION:
; APPLICANT: Greasley, Peter
; TITLE OF INVENTION: Cannabinoid Receptor
; FILE REFERENCE: ASZD-P01-752
; CURRENT APPLICATION NUMBER: US/10-521,420
; CURRENT FILING DATE: 2005-01-14
; PRIORITY APPLICATION NUMBER: SE 02022412-4
; PRIORITY FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 1
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-521-420-1

Query Match Similarity 100.0%; Pred. No. 5_je-215; Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0; Matches 472;

1 MKSILDGLADTTFRITTDLYVSGNDIQYEDIKGDMASKLGYFFQKPLTSFGSPFQE 60
1 MKSILDGLADTTFRITTDLYVSGNDIQYEDIKGDMASKLGYFFQKPLTSFGSPFQE 60
1 MKSILDGLADTTFRITTDLYVSGNDIQYEDIKGDMASKLGYFFQKPLTSFGSPFQE 60
1 KMTAGDNPOLYPADQVNITEFYNNKLSSPKEENENIQCGENFMIDECMVNLNPQLAIA 120
1 KMTAGDNPOLYPADQVNITEFYNNKLSSPKEENENIQCGENFMIDECMVNLNPQLAIA 120
1 VLSLTIGTFTVLENLVLVCYLHSRSLRCPSPHIGTSLAVADLIGSVIYVSFDFHV 180
1 VLSLTIGTFTVLENLVLVCYLHSRSLRCPSPHIGTSLAVADLIGSVIYVSFDFHV 180
1 HRQDSRNVELFKLGGSYTASPTAVSGLSTLTAAIARYISIHRPLAYKRIVTRPKAYAFCLM 240
1 HRQDSRNVELFKLGGSYTASPTAVSGLSTLTAAIARYISIHRPLAYKRIVTRPKAYAFCLM 240
1 HRQDSRNVELFKLGGSYTASPTAVSGLSTLTAAIARYISIHRPLAYKRIVTRPKAYAFCLM 240
1 WTIATIVAVPLLGNCBLSQCSDFPHIDETYLFWIGTVSYLLPIVYAMYILWK 300
1 WTIATIVAVPLLGNCBLSQCSDFPHIDETYLFWIGTVSYLLPIVYAMYILWK 300
1 WTIATIVAVPLLGNCBLSQCSDFPHIDETYLFWIGTVSYLLPIVYAMYILWK 300
301 AHSHAVMRIOGTQKSIILHTSEDERGVQTTRPDQARMAIRAKTIVLVLVLIICWGPLL 360
301 AHSHAVMRIOGTQKSIILHTSEDERGVQTTRPDQARMAIRAKTIVLVLVLIICWGPLL 360
301 AIMYDVFGKONKLIKTVFAFCMSMLCLNNTVNPITIALRSKDLRHAFRSMPPSCETGTAQ 420

; TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
; FILE REFERENCE: 018501-012500US
; CURRENT APPLICATION NUMBER: US/10/295,027
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 236
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-295-027-236

; Query Match 99.5%; Score 2412; DB 4; Length 472;
; Best Local Similarity 99.6%; Pred. No. 6.8e-214;
; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; SEQ ID NO: 1
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-764-425-168

Query Match 99.5%; Score 2412; DB 4; Length 472;
; Best Local Similarity 99.6%; Pred. No. 6.8e-214;
; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
; SEQ ID NO: 1
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-764-425-168

Query Match 99.5%; Score 2412; DB 4; Length 472;
; Best Local Similarity 99.6%; Pred. No. 6.8e-214;
; Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKSIIDGLADTFRTITDLYVGSNDIQYEDIKGDMASKLGYFQKFPLTSFRGSPFQE 60
Db 1 MKSIIDGLADTFRTITDLYVGSNDIQYEDIKGDMASKLGYFQKFPLTSFRGSPFQE 60
Qy 1 KMTAGDNPOLYPADQVNITEFYNKSLSPKBNENIQCENFMDFLCKWVNLPSCOLAIA 120
Db 1 KMTAGDNPOLYPADQVNITEFYNKSLSPKBNENIQCENFMDFLCKWVNLPSCOLAIA 120
Qy 1 VLSLTGTFTVLENILVCLHSSRLRCPSTPIGSALAVDILGSVITYSPIDFHVF 180
Db 1 VLSLTGTFTVLENILVCLHSSRLRCPSTPIGSALAVDILGSVITYSPIDFHVF 180
Qy 1 HRKDSRNVLFLKGCGTASFTASYGSFLTATARYISIRPLAYKRIVTRPKAVAFCLM 240
Db 1 HRKDSRNVLFLKGCGTASFTASYGSFLTATARYISIRPLAYKRIVTRPKAVAFCLM 240
Qy 1 121 VLSLTGTFTVLENILVCLHSSRLRCPSTPIGSALAVDILGSVITYSPIDFHVF 180
Db 1 121 VLSLTGTFTVLENILVCLHSSRLRCPSTPIGSALAVDILGSVITYSPIDFHVF 180
Qy 1 181 HRKDSRNVLFLKGCGTASFTASYGSFLTATARYISIRPLAYKRIVTRPKAVAFCLM 240
Db 1 181 HRKDSRNVLFLKGCGTASFTASYGSFLTATARYISIRPLAYKRIVTRPKAVAFCLM 240
Qy 1 181 PLDNMGDSDC1LHKHANNAASVRAESCIKSTVKLAKTMSVSTDTSAEAL 472
Db 1 181 PLDNMGDSDC1LHKHANNAASVRAESCIKSTVKLAKTMSVSTDTSAEAL 472
Qy 1 241 WTAIAIVAYLPGLGNNECEKLOSSVCSD1FPHIDBTYLMFWIGTVSLLFIVYAYMLWK 300
Db 1 241 WTAIAIVAYLPGLGNNECEKLOSSVCSD1FPHIDBTYLMFWIGTVSLLFIVYAYMLWK 300
Qy 1 241 WTAIAIVAYLPGLGNNECEKLOSSVCSD1FPHIDBTYLMFWIGTVSLLFIVYAYMLWK 300
Db 1 241 WTAIAIVAYLPGLGNNECEKLOSSVCSD1FPHIDBTYLMFWIGTVSLLFIVYAYMLWK 300

Qy 301 AHSHAVMRQRTQKSIIIIHSEDKYQVTRPQDMAIRLAKTVLILVYLIICGPLL 360
Db 301 AHSHAVMRQRTQKSIIIIHSEDKYQVTRPQDMAIRLAKTVLILVYLIICGPLL 360
Qy 361 ALMVYDFGRNKLKTVFAFCSMCLLNSTNPITYALRSKDLRHFRSMPSCGTQAQ 420
Db 361 ALMVYDFGRNKLKTVFAFCSMCLLNSTNPITYALRSKDLRHFRSMPSCGTQAQ 420
Qy 421 PLDNMGDSDC1LHKHANNAASVRAESCIKSTVKLAKTMSVSTDTSAEAL 472
Db 421 PLDNMGDSDC1LHKHANNAASVRAESCIKSTVKLAKTMSVSTDTSAEAL 472

RESULT 6
US-10-482-029-172
; Sequence 172, Application US/10482029
; Publication No. US20050037445A1
; GENERAL INFORMATION:
; APPLICANT: ODIN medical A/S
; TITLE OF INVENTION: Oncology drug innovation
; FILE REFERENCE: P 573 PC00
; CURRENT APPLICATION NUMBER: US/10/482,029
; CURRENT FILING DATE: 2003-12-29
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 172
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens

RESULT 5
US-10-764-425-168
; Sequence 168, Application US/10764425

Query Match 99.5%; Score 2412; DB 5; Length 472;
 Best Local Similarity 99.6%; Pred. No. 6.8e-214;
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKSLDGLADTTPTITDLYGSNDIYEDIKGDMASKLGYPQKPLTSRGSPEQE 60
 Db 1 MKSLDGLADTTPTITDLYGSNDIYEDIKGDMASKLGYPQKPLTSRGSPEQE 60
 Qy 61 KMTAGDNPOLVPAQVNTEPYNKSLSFKENEENIQGENFMDIECPMVNLPSQQLIA 120
 Db 61 KMTAGDNPOLVPAQVNTEPYNKSLSFKENEENIQGENFMDIECPMVNLPSQQLIA 120
 Qy 121 VLSLTIGPFTVLENLVLCVILHSURCRPSYHFIGSLAVADLGSVIFVYSPIDPHVF 180
 Db 121 VLSLTIGPFTVLENLVLCVILHSURCRPSYHFIGSLAVADLGSVIFVYSPIDPHVF 180
 Qy 181 HRKDSRNVLFLKGIGGTASFTASVGSLFLTATARYISIHRPLAYKRIVTRPKAVAFCLM 240
 Db 181 HRKDSRNVLFLKGIGGTASFTASVGSLFLTATARYISIHRPLAYKRIVTRPKAVAFCLM 240
 Qy 241 WTAIVAVLPLGGNCBKLQSVCSDFPHIDETYLFWIGTISVLLFIYVAYMYILWK 300
 Db 241 WTAIVAVLPLGGNCBKLQSVCSDFPHIDETYLFWIGTISVLLFIYVAYMYILWK 300
 Qy 301 AHSHAVRMHQRTQKSTIHTSEDGVQVTRDQARMAIRAKTLVLVVLICWGPPL 360
 Db 301 AHSHAVRMHQRTQKSTIHTSEDGVQVTRDQARMAIRAKTLVLVVLICWGPPL 360
 Qy 361 AIMVDYFGKONKLTKITVFAFCMSLCLNSTNPITYALRSKDLRAFRSMPSCEGTAQ 420
 Db 361 AIMVDYFGKONKLTKITVFAFCMSLCLNSTNPITYALRSKDLRAFRSMPSCEGTAQ 420
 Qy 421 PLDNMGDSDCLHKHANNAASVERAASCIKSTVKLAKVTMVSYSTDTSAEAL 472
 Db 421 PLDNMGDSDCLHKHANNAASVERAASCIKSTVKLAKVTMVSYSTDTSAEAL 472

RESULT 8

Qy 301 AHSHAVRMHQRTQKSTIHTSBDGKVQVTRDQARMAIRAKTLVLVVLICWGPPL 360
 Db 301 AHSHAVRMHQRTQKSTIHTSBDGKVQVTRDQARMAIRAKTLVLVVLICWGPPL 360
 . Qy 361 AIMVDYFGKONKLTKTAPCNSMLCLNSTNPITYALRSKDLRAFRSMPSCEGTAQ 420
 Db 361 AIMVDYFGKONKLTKTAPCNSMLCLNSTNPITYALRSKDLRAFRSMPSCEGTAQ 420
 Qy 421 PLDNMGDSDCLHKHANNAASVERAASCIKSTVKIAKVTMSYSTDTSAEAL 472
 Db 421 PLDNMGDSDCLHKHANNAASVERAASCIKSTVKIAKVTMSYSTDTSAEAL 472

RESULT 7

US-11-019-829-88
 ; Sequence 88, Application US/11019829
 ; Publication No. US0050136465A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoffmann-La Roche Inc.
 ; TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
 ; FILE REFERENCE: 22304
 ; CURRENT APPLICATION NUMBER: US/11/019,829
 ; CURRENT FILING DATE: 2004-12-22
 ; NUMBER OF SEQ ID NOS: 146
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO: 88
 ; LENGTH: 472
 ; TYPE: PRT
 ; FEATURE:
 ; NAME/KEY: cannabinoid receptor 1 (brain) variant 1
 ; LOCATION: (1)..(472)
 ; OTHER INFORMATION: LocusID: 1268; NM_016083
 US-11-019-829-88

Query Match 99.5%; Score 2412; DB 6; Length 472;
 Best Local Similarity 99.6%; Pred. No. 6.8e-214;
 Matches 470; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKSLDGLADTTPTITDLYGSNDIYEDIKGDMASKLGYPQKPLTSRGSPEQE 60
 Db 1 MKSLDGLADTTPTITDLYGSNDIYEDIKGDMASKLGYPQKPLTSRGSPEQE 60
 Qy 61 KMTAGDNPOLVPAQVNTEPYNKSLSFKENEENIQGENFMDIECPMVNLPSQQLIA 120
 Db 61 KMTAGDNPOLVPAQVNTEPYNKSLSFKENEENIQGENFMDIECPMVNLPSQQLIA 120
 Qy 121 VLSLTIGPFTVLENLVLCVILHSURCRPSYHFIGSLAVADLGSVIFVYSPIDPHVF 180
 Db 121 VLSLTIGPFTVLENLVLCVILHSURCRPSYHFIGSLAVADLGSVIFVYSPIDPHVF 180
 Qy 181 HRKDSRNVLFLKGIGGTASFTASVGSLFLTATARYISIHRPLAYKRIVTRPKAVAFCLM 240
 Db 181 HRKDSRNVLFLKGIGGTASFTASVGSLFLTATARYISIHRPLAYKRIVTRPKAVAFCLM 240
 Qy 241 WTAIVAVLPLGGNCBKLQSVCSDFPHIDETYLFWIGTISVLLFIYVAYMYILWK 300
 Db 241 WTAIVAVLPLGGNCBKLQSVCSDFPHIDETYLFWIGTISVLLFIYVAYMYILWK 300

Qy 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDOARMAIRAKTIVLVLVLLCWPGLL 360
 Db 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDQARMDIRLKCTVLVLVLLCWPGLL 360

RESULT 10
 US-10-295-027-238
 ; Sequence 238, Application US/10295027
 ; Publication No. US2003023350A1

Qy 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420
 Db 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420

Qy 421 PLDNMSGDSCLHKHANNAASVRAEASCIKSTVKIAKTMVSVDTSABAL 472
 Db 421 PLDNMSGDSCLHKHANNAASVRAEASCIKSTVKIAKTMVSVDTSABAL 472

RESULT 9
 US-10-925-095-469
 ; Sequence 469, Application US/10925095
 ; Publication No. US20050019840A1

GENERAL INFORMATION:
 APPLICANT: Lin, I-Lin
 APPLICANT: Lehmahn-Bruinsma, Karin
 APPLICANT: Liaw, Chen W.
 APPLICANT: Lin, I-Lin
 TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G Protein-Coupled Receptors
 FILE REFERENCE: AREN-207
 CURRENT APPLICATION NUMBER: US/10/925, 095
 CURRENT FILING DATE: 2004-08-24
 PRIOR APPLICATION NUMBER: US/09/826, 509
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/195, 747
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: 09/170, 496
 PRIOR FILING DATE: 1998-10-13
 NUMBER OF SEQ ID NOS: 589
 SOFTWARE: PatentIn Version 2.1
 SEQ ID NO: 469
 LENGTH: 472
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-925-095-469

Query Match 99.3%; Score 2407; DB 5; Length 472;
 Best Local Similarity 99.4%; Pred. No. 2e-213; 3; Indels 0; Gaps 0;
 Matches 469; Conservative 0; Mismatches 0;

Qy 1 MKSILDGADFTTTDLYVGNSNDIQEPIKGDMASKLGYPKPKPLTSFRGSPFQE 60
 Db 1 MKSILDGADFTTTDLYVGNSNDIQEPIKGDMASKLGYPKPKPLTSFRGSPFQE 60

Qy 61 KNTAGDNPQLVPADQVNITEFYNSKLSFKENBENTOCGENFMDIEFVNLPNSQOLIA 120
 Db 61 KNTAGDNPQLVPADQVNITEFYNSKLSFKENBENTOCGENFMDIEFVNLPNSQOLIA 120

Qy 121 VLSLTLCPTVLENLVLCVILHSRSLRCPSYHEFIGSLAYADLGSSVITYFSIDFHVF 180
 Db 121 VLSLTLCPTVLENLVLCVILHSRSLRCPSYHEFIGSLAYADLGSSVITYFSIDFHVF 180

Qy 181 HKDSRNVLFLKGGVTSFTAVGSGFLTARYIYHRPLAYKRIVTRPAWAFCLM 240
 Db 181 HKDSRNVLFLKGGVTSFTAVGSGFLTARDYIYHRPLAYKRIVTRPAWAFCLM 240

Qy 241 WTAIAVAVPLPLGWNCKLQSVCSDPHIDETYLFWIGTVSLLFIVYAMYILWK 300
 Db 241 WTAIAVAVPLPLGWNCKLQSVCSDPHIDETYLFWIGTVSLLFIVYAMYILWK 300

Qy 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDQARMAIRAKTIVLVLVLLCWPGLL 360
 Db 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDQARMAIRAKTIVLVLVLLCWPGLL 360

Qy 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420
 Db 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420

Qy 421 PLDNMSGDSCLHKHANNAASVRAEASCIKSTVKIAKTMVSVDTSABAL 472
 Db 421 PLDNMSGDSCLHKHANNAASVRAEASCIKSTVKIAKTMVSVDTSABAL 472

RESULT 10
 US-10-295-027-238
 ; Sequence 238, Application US/10295027
 ; Publication No. US2003023350A1

GENERAL INFORMATION:
 APPLICANT: Afar, Daniel
 APPLICANT: Aziz, Natasha
 APPLICANT: Giabsberg, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Hevezsi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: Bos Biotechnology, Inc.

TITLE OF INVENTION: Methods of Screening for Modulators of Cancer Compositions and Methods of Diagnosis of Cancer, Compositions and Methods of Screening for Modulators of Cancer

FILE REFERENCE: 018501012500US
 CURRENT APPLICATION NUMBER: US/10/295, 027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663, 733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350, 666
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335, 394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332, 464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334, 393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340, 376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347, 211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347, 349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355, 250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356, 714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SEQ ID NO: 238
 LENGTH: 472
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-238

Query Match 99.1%; Score 2401; DB 4; Length 472;
 Best Local Similarity 98.9%; Pred. No. 7.1e-213; 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MKSILDGADFTTTDLYVGNSNDIQEPIKGDMASKLGYPKPKPLTSFRGSPFQE 60
 Db 1 MKSILDGADFTTTDLYVGNSNDIQEPIKGDMASKLGYPKPKPLTSFRGSPFQE 60

Qy 121 VLSLTLCPTVLENLVLCVILHSRSLRCPHYFGSLAVADLGSSVITYFSIDFHVF 180
 Db 121 VLSLTLCPTVLENLVLCVILHSRSLRCPHYFGSLAVADLGSSVITYFSIDFHVF 180

Qy 241 WTAIAVAVPLPLGWNCKLQSVCSDPHIDETYLFWIGTVSLLFIVYAMYILWK 300
 Db 241 WTAIAVAVPLPLGWNCKLQSVCSDPHIDETYLFWIGTVSLLFIVYAMYILWK 300

Qy 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDQARMAIRAKTIVLVLVLLCWPGLL 360
 Db 301 AHSHAVRMIORGTOKSIIHTSBDGKVQTRDQARMAIRAKTIVLVLVLLCWPGLL 360

Qy 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420
 Db 361 AIMVYDFGKONKLKTVFACSMCLINSTVNPIYALRSKDLRHAFRSMFSPCEGTAQ 420

Qy	241 WTIATIVAYPLPLGWCNCEKLSQSYCSDDPHIDETYLFWIGTTSVLLFIVYAMYILWK 300	Db	24 STTKSENEENIQGENFM DIECFMVLNPSSQALIAVSLTGFTYLENLVLCVILHS 83
Db	241 WTIATIVAYPLPLGWCNCEKLSQSYCSDDPHIDETYLFWIGTTSVLLFIVYAMYILWK 300	Qy	145 RSLRCPSYHFQGSVALADLGSIVFYSFIDFHVKRDSDNFVPLKGTYTASFTAV 204
Qy	301 AHSHAVRMQORTOKSIIHTSDEGKVQTRPDAQMAIRLAKTLVLLVLLICWGPPL 360	Db	84 RSLRCPSYHFQGSVALADLGSIVFYSFIDFHVKRDSDNFVPLKGTYTASFTAV 143
Db	301 AHSHAVRMQORTOKSIIHTSDEGKVQTRPDAQMDIRLAKTLVLLVLLICWGPPL 360	Qy	205 GSFLPTIARYISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 264
Qy	361 AIMYDVGIONKLKTTFAFCMSLCLNSTNPVIALRSQDLRHARSMPSCEGTAQ 420	Db	144 GSFLPTAIDRVISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 203
Db	361 AIMYDVGICKONKLKTTFAFCMSLCLNSTNPVIALRSQDLRHARSMPSCEGTAQ 420	Qy	265 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 324
Qy	421 PLDNMGDSDCLHKHANNAVSRAECKSTKVIKAVTMVSSTDSEAEL 472	Db	204 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 263
Db	421 PLDNMGDSDCLHKHANNAVSRAECKSTKVIKAVTMVSSTDSEAEL 472	Qy	325 GKQVTRPDQARMAIRLAKTLVLLVLLICWGPPLAIMYDVFGRNKLKTVFAFCSM 384
Qy	RESULT 191 US-10-295-027-240	Db	264 GKQVTRPDQARNDIRLAKTLVLLVLLICWGPPLAIMYDVFGRNKLKTVFAFCSM 323
Qy	Sequence 240, Application US/10295027	Qy	385 LCILNSTNPVIALRSKDLRHAFRSMPSCEGTAQPLDNMGDSDCLHKHANNAVSVR 444
Qy	Publication No. US20030232350A1	Db	324 LCILNSTNPVIALRSKDLRHAFRSMPSCEGTAQPLDNMGDSDCLHKHANNAVSVR 383
GENERAL INFORMATION:		Qy	445 AAESCIKSTVKIAKTMVSSTDSEAEL 472
APPLICANT: Afar, Daniel		Db	384 AAESCIKSTVKIAKTMVSSTDSEAEL 411
APPLICANT: Aziz, Natasha			
APPLICANT: Ginsberg, Wendy M.			
APPLICANT: Gish, Kurt C.			
APPLICANT: Glynn, Richard			
APPLICANT: Hevezsi, Peter A.			
APPLICANT: Mack, David H.			
APPLICANT: Murray, Richard			
APPLICANT: Watson, Susan R.			
APPLICANT: Eos Biotechnology, Inc.			
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and			
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer			
FILE REFERENCE: 0185-01-012500US			
CURRENT APPLICATION NUMBER: US/10/295,027			
CURRENT FILING DATE: 2002-11-13			
PRIOR APPLICATION NUMBER: US 09/663,733			
PRIOR FILING DATE: 2000-09-15			
PRIOR APPLICATION NUMBER: US 60/350,666			
PRIOR FILING DATE: 2001-11-13			
PRIOR APPLICATION NUMBER: US 60/335,394			
PRIOR FILING DATE: 2001-11-15			
PRIOR APPLICATION NUMBER: US 60/332,464			
PRIOR FILING DATE: 2001-11-21			
PRIOR APPLICATION NUMBER: US 60/334,393			
PRIOR APPLICATION NUMBER: US 60/340,376			
PRIOR FILING DATE: 2001-12-14			
PRIOR APPLICATION NUMBER: US 60/347,211			
PRIOR FILING DATE: 2002-01-08			
PRIOR APPLICATION NUMBER: US 60/347,349			
PRIOR FILING DATE: 2002-01-10			
Remaining Prior Application data removed - See File Wrapper or PALM.			
NUMBER OF SEQ ID NOS: 1386			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO: 240			
LENGTH: 411			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-295-027-240			
Qy	85 SLSSFKNEENIQGENFM DIECFMVLNPSSQALIAVSLTGFTYLENLVLCVILHS 144	Qy	85 SLSSFKNEENIQGENFM DIECFMVLNPSSQALIAVSLTGFTYLENLVLCVILHS 144
Db	84 RSLRCPSYHFQGSVALADLGSIVFYSFIDFHVKRDSDNFVPLKGTYTASFTAV 143	Db	84 RSLRCPSYHFQGSVALADLGSIVFYSFIDFHVKRDSDNFVPLKGTYTASFTAV 143
Qy	205 GSFLPTIARYISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 264	Qy	205 GSFLPTAIDRVISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 203
Db	144 GSFLPTAIDRVISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 203	Db	144 GSFLPTAIDRVISIHRPLAYKRIVTRPKAVVAFCLMPTIAVIALPLLGNCNEKLSQSC 203
Qy	265 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 324	Qy	265 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 324
Db	204 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 263	Db	204 SDIFPHIDETYLFWIGTTSVLLFIVYAMYILWKAHSHAVRMQRTOKSIIHTSED 263
Qy	325 GKQVTRPDQARMAIRLAKTLVLLVLLICWGPPLAIMYDVFGRNKLKTVFAFCSM 384	Qy	325 GKQVTRPDQARMAIRLAKTLVLLVLLICWGPPLAIMYDVFGRNKLKTVFAFCSM 384

RESULT 13
 US-11-019-829-89
 Sequence 99, Application US/11019829
 Publication No. US20050136465A1
 GENERAL INFORMATION:
 APPLICANT: Hoffmann-La Roche Inc.
 TITLE OF INVENTION: Novel targets for obesity from subcutaneous fat
 FILE REFERENCE: 22304
 CURRENT APPLICATION NUMBER: US/11/019, 829
 CURRENT FILING DATE: 2004-12-22
 NUMBER OF SEQ ID NOS: 146
 SEQ ID NO: 89
 LENGTH: 411
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: cannabinoid receptor 1 (brain) variant 2
 LOCATION: (1)..(411)
 OTHER INFORMATION: LocusID: 1268; NM_033181
 US-11-019-829-89

Query Match 80.6%; Score 1954; DB 6; Length 411;
 Best Local Similarity 98.5%; Pred. No. 1..2e-171;
 Matches 382; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 85 SLSKTKSENEENIQGENFMDIECFMVNLNPSCOLAIVAVSLTIGETVYLENIVLVCVILHS 144
 Db 24 STKTSKSENEENIQGENFMDIECFMVNLNPSCOLAIVAVSLTIGETVYLENIVLVCVILHS 83

Qy 145 RSLRCRSYHPTGSLAVADLGSSVIVYSPIDFAYFRKDSRNVLPLKGCVTAFTASV 204
 Db 84 RSLRCRSYHPTGSLAVADLGSSVIVYSPIDFAYFRKDSRNVLPLKGCVTAFTASV 143

Qy 205 GSFLFLTVIARYTISIHRPLAYKRIVTRKAVVAFCLMVTIAVAVLPLLGNCBLSQVC 264
 Db 144 GSFLFLTADRYTISIHRPLAYKRIVTRKAVVAFCLMVTIAVAVLPLLGNCBLSQVC 203

Qy 265 SDIFPHDDETYLMFWIGTTSVLLFLTVIAYMYLWKAHSHAVRMIGRGTOKSIIHTSED 324
 Db 204 SDIFPHDDETYLMFWIGTTSVLLFLTVIAYMYLWKAHSHAVRMIGRGTOKSIIHTSED 263

Qy 325 GRVQVTPDQARMAIRAKTIVLVLVLUICGPMKLNKIKTVFAPCSM 384
 Db 264 GRVQVTPDQARMDIRAKTIVLVLVLUICGPMKLNKIKTVFAPCSM 323

Qy 385 LCILNSTVNPIIYLRSKDLRHAFRSMPPSCGEAQPLDNMGDSDLKHANNASVHR 444
 Db 324 LCILNSTVNPIIYLRSKDLRHAFRSMPPSCGEAQPLDNMGDSDLKHANNASVHR 383

Qy 445 AAECKISTVKIAKTIVMSVSTDSTAEL 472
 Db 384 AAECKISTVKIAKTIVMSVSTDSTAEL 411

; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burner, Christine L.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225, 567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIORITY FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2232
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 86
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-225-567A-86

Query Match 29.3%; Score 710; DB 4; Length 360;
 Best Local Similarity 45.2%; Pred. No. 8..7e-57;
 Matches 149; Conservative 57; Mismatches 94; Indels 30; Gaps 6;

Qy 78 ITSFYNKSLSSPKKENENIQGENFNDIECFMVNLNPSCOLAIVAVSLTIGETVYLENLY 137
 6 VTEIANGSKDGLDSN-----PMKDYMISGPQKTAVALCTLGSLSALENVAV 54

Qy 138 LCVLTHSRSLCRSYHPTGSLAVADLGSSVIVYSPIDFAYFRKDSRNVLPLKGCVT 197
 55 LYLLSHQURRKPSYFIGSLAGDFLAVSVFACSFVNHFVPGCVDSKAVFLKIGSVT 114

Db 198 ASFTASVGSLFLTATARYTISIHRPLAYKRIVTRKAVVAFCLMVTIAVAVLPLLGWCN 257
 115 MTFTASVGSLSLTLADRYLCLRYPSKAKLTGRALVLTGIMWVSLAVSYSLPLMGWTC 174

Qy 258 EKLQSYCSDFEPHDDETYLMFWIGTTSVLLFLTVIAYMYLWKAHSHAVRMIGRGTOKSII 317
 175 --CPRPCSEDFPLPNPDYLSWMLPISAFPSGITYGHVLWKAHQHVA-----SL 223

Qy 318 IHTTSEDKYQVTRPQDQARMA-IRLAKTIVLVLVLUICGPMKLNKIKTVFAPCSM 375
 224 SGH--QDRQV---FGMARNRLDVRALKTIVLGLVLAFLICWPFPTLMAHSLATLSDQV 277

Db 376 KTVFAFCSMCLLNSTVNPIIYARSKDLR 405
 278 KCAFAFCSMCLLNSTVNPIIYARSGEIR 307

RESULT 15
 US-10-290-078-3
 Sequence 3, Application US/102900078
 ; Publication No. US20030124596A1
 ; GENERAL INFORMATION:
 APPLICANT: Carroll, Joseph A.
 ; TITLE OF INVENTION: Methods and Compositions for Treating
 ; Hematological Disorders Using 232, 2059, 10630, 12848, 13875,
 ; TITLE OF INVENTION: 14395, 14618, 17692 or 58874
 ; FILE REFERENCE: MPI01-288P1 (M)
 ; CURRENT APPLICATION NUMBER: US/10/280, 078
 ; CURRENT FILING DATE: 2002-11-07
 ; NUMBER OF SEQ ID NOS: 27
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 360
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-290-078-3

Query Match 29.3%; Score 710; DB 4; Length 360;
 Best Local Similarity 45.2%; Pred. No. 8..7e-57;
 Matches 149; Conservative 57; Mismatches 94; Indels 30; Gaps 6;

Qy 78 ITSFYNKSLSSPKKENENIQGENFNDIECFMVNLNPSCOLAIVAVSLTIGETVYLENLY 137
 6 VTEIANGSKDGLDSN-----PMKDYMISGPQKTAVALCTLGSLSALENVAV 54

RESULT 14
 US-10-225-567A-86
 ; Sequence 86, Application US/10225567A
 ; Publication No. US2003011379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lifespan Biosciences

QY	138	LCVILHSSRLCRPSYHFTGSLAVADLIGSVIFVSPIDFHYFRKDSRNVEFLKUGGV	197
DB	55	LYLISSHLQRKESYLFIGSLAGDFASVVACSFNFAYPHGDSKAEFLKGSVT	114
QY	198	ASPTASVGSSLTAIARYSTISRPLAYKRIVTRPKAVAFCLMTIAVIAVPLIGMNC	257
DB	115	MTPASVGSSLTAIDRTICLRYPPSYCALLTGRALTYLGIMWLSALVSTPLMGWTC	174
QY	258	EKQOSVCSDFPHIDETIMFWIGVTSVLLFIYAMYLWKAHSARVMQRTOKSI	317
DB	175	-CPRPCSELFFPLIPNDVLLSWLFAIFSGIYTIGHVLWKAHORVA-----SL	223
QY	318	IHTSEDGRKVQTRPDAQMA - IRLAKTLVLLIVVLLICWGPLLAINVYDVFKNKLII	375
DB	224	SGH - QDRQV - - PGMARMLDVRLAATLGLVAVLICWPFLAMAHSLATTLSQV	277
QY	376	KTVFAFCSMCLCINSTVNPITYAURSKDLR	405
DB	278	KKAAFAFCSMCLNSMNPVIAURSGIER	307

Search completed: January 6, 2006, 21:16:59
 Job time : 173 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	2412	99.5	472	S17595	cannabinoid receptor CB1 - human
2	2343.5	96.3	473	A33117	C;Species: Homo Sapiens (man)
3	734.5	30.3	347	S670364	C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
4	706	29.1	360	S36750	C;Accession: S17595; GI: 55879; Reference number: S13668; PMID:9088103; PMID:1718258
5	363	15.0	364	JCS293	A;Title: Molecular cloning of a human cannabinoid receptor which is also expressed in t
6	353	14.6	381	AJ5300	A;Reference number: S17595; A;Accession: S17595
7	348.5	14.4	362	JCT559	A;Molecule type: mRNA
8	346.5	14.3	378	JCS245	A;Residues: 1-472 <GER1>
9	340	14.0	383	IS3870	A;Cross-references: UNIPARC:UPI00000008AA; EMBL:X54937; NID:929914; PI
10	306.5	12.6	477	S71323	R;Shire, D.; Carillon, C.; Vassart, G.; Parmentier, M.
11	305	12.6	325	JC2193	R;Gerard, C.; Molletereau, C.; Vassart, G.; Parmentier, M.
12	304	12.5	372	J49008	A;Title: Nucleotide sequence of a human cannabinoid receptor cDNA.
13	295.5	12.2	352	JCL465	A;Reference number: S13668; PMID:2263478
14	295	12.2	330	S40454	A;Accession: S13668
15	292	12.0	325	I46416	A;Status: translation not shown
16	290.5	12.0	466	A35375	A;Molecule type: mRNA
17	289	11.9	330	A55689	A;Residues: 1-124 <SHI>
18	288.5	11.9	363	S48697	A;Cross-references: UNIPARC:UPI000017COAC; GB:X81120
19	285.5	11.8	297	C41265	C;Genetics:
20	285	11.8	466	I57959	A;Gene: GDB:CNR1; OMIM:114610
21	283	11.7	429	S65656	A;Cross-position: 6q14-6q15
22	283	11.7	466	JN0765	C;Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
23	283	11.7	499	S65657	F;117-142/Domain: transmembrane #status predicted <TM1>
24	281	11.6	360	B46647	F;155-175/Domain: transmembrane #status predicted <TM2>
25	280	11.6	266	I65990	F;188-212/Domain: transmembrane #status predicted <TM3>
26	280	11.6	515	A40491	F;233-256/Domain: transmembrane #status predicted <TM4>
27	277	11.4	517	A45121	F;275-299/Domain: transmembrane #status predicted <TM5>
28	276	11.4	314	S71420	F;345-365/Domain: transmembrane #status predicted <TM6>
29	276	11.4	314	S70005	F;378-399/Domain: transmembrane #status predicted <TM7>

Db	1 MKSILDGLADTTFRITITDLYVGNSNDIYEDIKGDMASKLGYFPQQKPLTSRGSPPQE 60	Db	181 FHRKSDSPVFLFKGGTASFTAVGSISFLTAIRYKRVTRPAAVAFCL 240
Qy	61 KMTAGDNIPOLYPQAQNTEFYNKSLSSPKENEEENIQGENFMEDIECTMVLNPSQQLAI 120	Qy	240 MTTIAIVAVLPFLGHNCEKLOSVCSDFPHDETYLMFWIGTYSVLLFLIVYAYMMYLW 299
Db	61 KMTAGDNIPOLYPQAQNTEFYNKSLSSPKENEEENIQGENFMEDIECTMVLNPSQQLAI 120	Db	241 MTTIAIVAVLPFLGHNCKLQSVCSDFPLIDETYLMFWIGTYSVLLFLIVYAYMMYLW 300
Qy	121 VLSLTIGTFVLENLVLICVILHRSRSLCRPSYHFIGSLAVADLGSYIFVTSFIDFFVF 180	Qy	300 KAISHAVRMIQRTQKSLLIHTSEDGKVQTREPDQARMAIRLAKTLVLLVLLICMGPL 359
Db	121 VLSLTIGTFVLENLVLICVILHRSRSLCRPSYHFIGSLAVADLGSYIFVTSFIDFFVF 180	Db	301 KAISHAVRMIQRTQKSLLIHSBGGKVQTREPDQARMDIRLAKTLVLLVLLICMGPL 360
Qy	181 HRDSRNVFLFKLGTVTASFTAVGSLLTATAARYIISHRPLAYKRITVRPAAVAFCLM 240	Qy	360 LAIMYDVFGRKNNKLKITYVAFCSMLCLNSTNPYIYALRSKDLRHAFRSMFSCGTA 419
Db	181 HRDSRNVFLFKLGTVTASFTAVGSLLTATAARYIISHRPLAYKRITVRPAAVAFCLM 240	Db	361 LAIMYDVFGRKNNKLKITYVAFCSMLCLNSTNPYIYALRSKDLRHAFRSMFSCGTA 420
Qy	241 WTAIVAVLPFLGHNCEKLOSVCSDFPHDETYLMFWIGTYSVLLFLIVYAYMMYLW 300	Qy	420 QPLDNMGSDSDCLHKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAAEL 472
Db	241 WTAIVAVLPFLGHNCEKLOSVCSDFPHDETYLMFWIGTYSVLLFLIVYAYMMYLW 300	Db	421 QPLDNMGSDSDCLHKHANNTASHRAAESCIKSTVKIAKVTMSVSTDTSAAEL 473
Qy	301 AHSHAVRMIQRTQKSIIHTTSEDGKVQTREPDQARMAIRLAKTLVLLVLLICMGPL 360	RESULT 3	
Db	301 AHSHAVRMIQRTQKSIIHTTSEDGKVQTREPDQARMDIRLAKTLVLLVLLICMGPL 360	Db	S70364
cannabinoid receptor CB2, peripheral - mouse			
Qy	361 AIMYDVFGRKNNKLKITYVAFCSMLCLNSTNPYIYALRSKDLRHAFRSMFSCGTAQ 420	N: Alternative names: G protein-coupled receptor CB2	
Db	361 AIMYDVFGRKNNKLKITYVAFCSMLCLNSTNPYIYALRSKDLRHAFRSMFSCGTAQ 420	C:Species: Mus musculus (house mouse)	
Qy	421 PLDNMGSDCLHKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAAEL 472	C:Accession: S70364; S54163	
Db	421 PLDNMGSDCLHKHANNAASVHRAAESCIKSTVKIAKVTMSVSTDTSAAEL 472	C:Sequence_revision: 09-May-1997 #text_change 09-Jul-2004	
Best Local Similarity 48.2%; Pred. No. 3.8e-53; Matches 150; Conservative 53; Mismatches 89; Indels 19; Gaps 4;			
Qy	301 AHSHAVRMIQRTQKSIIHTTSEDGKVQTREPDQARMAIRLAKTLVLLVLLICMGPL 360	Qy	99 GENFMIDBCFMVLTNPSCQOLATAVLSLTIGTFTVLENLVLCYTLHSRSLRCPSPYHFIGS 158
A: Molecule type: mRNA			
A: Residues: 1-347 <SH1>	A: Cross-references: UNIPROT:P47936; UNIPARC:UPI0000019CB; EMBL:X06405; NID:9791081; PI:R/Shire, D.; Calandra, B.; Rinaldi-Carmona, M.; Oustric, D.; Pessegu, B.; Bonnin-Caban, R.; Shire, D.; Calandra, B.; Rinaldi-Carmona, M.; Oustric, D.; Pessegu, B.; Bonnin-Caban, Biochim. Biophys. Acta 1307, 132-136, 1996	C: Superfamily: melanocortin receptor	C:Keywords: G protein-coupled receptor; glycoprotein; transmembrane protein
A: Title: Molecular cloning, expression and function of the murine CB2 peripheral cannabinoid receptor	A:Title: Structure of a cannabinoid receptor and functional expression of the cloned cDNA	Query Match Score 734.5 ; DB 2 ; Length 347;	
A: Reference number: A33117; PMID:9032039; PMID:2165569	A:Accession: A33117	Best Local Similarity 48.2%; Pred. No. 3.8e-53; Matches 150; Conservative 53; Mismatches 89; Indels 19; Gaps 4;	
A: Accession: A33117	A: Molecule type: mRNA	Qy	16 GLBNPNEKYMILSGQOIAVAVLCTMGLLSALENNAVLYLSSRLRKFPSYLFISS 75
A: Residues: 1-473 <MAT>	A: Cross-references: Uniprot:P20222; Uniparc:UPI000012710C; GB:X55812; NID:91552375; PID:N	Db	159 LAVADLGSVIFTYFSDFDHUFHRKDSRNVLFLKGYTASFTAVSGLSLFTAIARYTISI 218
R/Shire, D.; Carillon, C.; Kaghadj, M.; Calandra, B.; Rinaldi-Carmona, M.; Le Fur, G.; Ca J. Biol. Chem. 270, 3726-3731, 1995	C:Accession: A33117; C55879	Db	76 LAGDAFLASVIFACNFVIFHVPFGVDSNAIFLKGYSWTFAVSCLLTAVDRYLCL 135
A: Title: An amino-terminal variant of the central cannabinoid receptor resulting from al	A: Status: preliminary; not compared with conceptual translation	Qy	219 HRPFLAKVTRKAVAFCLWTIAVPLGLWCEKLSQVCSDFIFPHADETYLMF 278
A: Reference number: A33117; PMID:95181329; PMID:7876112	A: Molecule type: mRNA	Db	136 CPPPTKAKVTRGRALVALCWNVMSLALISYPLMGWTIC-CPSPCSELFPLIPNDYLIG 193
A: Accession: C55879	A: Residues: 1-107 <SH1>	Qy	279 WIGTSVLLFLIVYAYMYLWKAHSHAVRMIQRTQKSIIHTTSEDGKVQVTRPDAOARMA 338
A: Cross-references: Uniparc:UPI000017C8D8	C:Keywords: G protein-coupled receptor; glycoprotein; membrane protein	Db	194 WLIJFATLFSGITYTYGVILWAQHRYATLB-----QDRV-----PGIARM 238
Qy	1 MKSILDGLADTTFRITITDLYVGNSNDIYEDIKGDMASKLGYFPQQKPLTSRGSPPQE 60	Qy	339 --IRLAKTLVLLVLLICMGPPLAIMYDVFGKMKLIKIVYAFCSMLCLNSTVNPII 396
Db	1 MKSILDGLADTTFRITITDLYVGNSNDIYEDIKGDMASKLGYFPQQKPLTSRGSPPQE 60	Db	239 LDYRLAKTLVLLVLLICWFPALMGHSLVTTLSQVKEAFCSMLCLTNVNPII 298
RESULT 4		cannabinoid receptor CB2 - human	
Qy	61 KMTAGDNIPOLYPQAQNTEFYNKSLSSPKENEEENIQGENFMEDIECTMVLNPSQQLAI 119	N: Alternative names: cannabinoid receptor CB2 - human	
Db	61 KMTAGDNIPOLYPQAQNTEFYNKSLSSPKENEEENIQGENFMEDIECTMVLNPSQQLAI 120	C:Species: Homo sapiens (man)	
Qy	120 AVSLTIGTFVLENLVLICVILHRSRSLCRPSYHFIGSLAVADLGSYIFVTSFIDFHV 179	C:Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999	
Db	121 AVSLTIGTFVLENLVLICVILHRSRSLCRPSYHFIGSLAVADLGSYIFVTSFIDFHV 180		
Qy	180 FHRDSRNVFLFKLGTVTASFTAVGSLLTATAARYIISHRPLAYKRITVRPAAVAFCL 239		

C;Accession: S36750	R;Residues: 1-360 <MUN>	A;Cross-references: UNIPARC:UPI00001789D5; EMBL:X74328	C;Superfamily: melanocortin receptor	Db	111 PNTTRLTSTWLLRQGLDTSLSRVANLIAIERHTTVPRMQLHTRMSNR-RVWWVVIV 169
Nature: 35%, 61-65, 1993	A;Title: Molecular characterization of a peripheral receptor for cannabinoids.	A;Reference number: S36750; MUID:93368659; PMID:7689702	A;Accession: S36750	Qy	239 LMNTTAIAAVLPLGNCNCEKLUQSVCSDFIPLPHIDETYLFWIGTTSVLLFIVYAYMYL 298
A;Status: Preliminary	A;Molecule type: mRNA	C;Superfamily: melanoctin receptor	Db	170 VIWTMAIVGAIPSGWNCCIDTNCNNAPLYDSVLAFLWFAATFLNLTVPTVMVLYAHIF 229	
A;Residues: 1-360 <MUN>	A;Cross-references: UNIPARC:UPI00001789D5; EMBL:X74328	C;Superfamily: melanocortin receptor	Qy	299 WKAISHAVRMIQRTQTKSIIHTSEDGKVQVTRDQAMAIRAKTLVLLVUVLICWGP 358	
Query Match Score: 29.1%; Best Local Similarity: 44.8%; Matches: 148; Conservativeness: 57; Niematches: 95; Indels: 30; Gaps: 6;	Score: 706; Pred. No. 9.1e-51; Nismatches: 57; Niematches: 95; Indels: 30; Gaps: 6;	Db	230 GYVRQRTMMSR-----HSGPQRNRDIT-----MMSSLKTWVIVLGASTICWTP 273		
Qy	78 ITEFYNSKLSSPKKENEEENIQCQGENFDIECEMVLNPSQIAAVLSSLTUGFTVLENLV 137	Db	359 LLAINMVYDVFGKNNRLIKTVFAGFSMCLLNSTNPITYALRSIDRLRAFRSMPPSCEGT 418		
Db	6 VTEIANGSKGQLDSDN-----PMKDMILSGPQTKAVAVLCTLGSLAENVAV 54	Qy	274 GLVLLLDVCCPQCDVL-AVEKFPLLLABFNSAMNPYIYSDKEMSATFQIL-----C 327		
Qy	138 ICVLHRSRSLCRPSYHFIGSLSLAVADLIGSVIYTSFDPFHKRDSRNVEFLPKLGCVT 197	Db	419 AQPDLNSMGEDSDCILKHANN-----AASTVHRAABSCI 450		
Db	55 LYLISSHQURKPKSTLFIGSLAGDAFLASVVFACSFVNPHVFRGVDSKAVFLUKIGSVT 114	Db	328 CQRSENPTGETTESDRSASSLNLHTLAGVHSNDSSV 364		
Qy	198 ASPTAISVGSLPLTIAIYIISHTRPLAYKRVTRPKAVAFCLMTTIAAVLPLGNC 257	RESULT 6			
Db	115 MTFTIASVGSLLTADRYLICRYPSSYKALLTRGRGYLTGIMAVSULSYLPGMGK 174	A35300	A;Cross-references: UNIPROT:P21453; UNIPARC:UPI0000037801; GB:W31210; NID:9181948; PIDN:		
Qy	258 EKLQSYCSDIPPHIDETYLFWIGTTSVLLFIVYAYMYLWKAISHAVRMIQRTQKS 317	C;Species: Homo sapiens (man)	C;Species: Homo sapiens (man)		
Db	175 --CPRCSEFLPLIPDYLISWLFLAPLPGSIITYGHVWKAHOVA-----SL 223	C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004	C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004		
Qy	318 IIHTSEDGKVQVTRDQAMAR-IRIATKTYLVLVLLVUICNGPUJAIIMYYDVFGMKNKLJ 375	R;Hlia, T.; Maciaig, T.	R;Hlia, T.; Maciaig, T.		
Db	224 SGH--QDQV---PEGRARMLDVRIAKTYLVLVLLVLCWFPVIALMAHSLATTLSQDV 277	A;Gene: GDB:127754; OMIM:131222	J. Biol. Chem. 265, 9308-9313, 1990		
Qy	376 KIVFAPCSMCLLNSTNPITYALRSKDL 405	A;Cross-references: GDB:127754; OMIM:131222	A;Title: An abundant transcript induced in differentiating human endothelial cells encc		
Db	278 KKAPAFCSMCLLNSTNPVYALRSGEIR 307	A;Map position: 2q13-2q13	A;Reference number: A35300; MUID:90264425; PMID:2160972		
RESULT 5		C;Accession: A35300	C;Accession: A35300		
JCS293	lysophosphatidic acid receptor - human	A;Molecule type: mRNA	A;Molecule type: mRNA		
N;Alternative names: Edg2 protein	C;Species: Homo sapiens (man)	A;Cross-references: GDB:ECGF1	A;Cross-references: GDB:ECGF1		
C;Date: 16-Apr-1997 #sequence_revision 09-May-1997	C;Species: Homo sapiens (man)	A;Gene: GB:ECGF1	C;Genetics:		
C;Accession: JCS293	C;Date: 16-Apr-1997 #sequence_revision 09-May-1997	A;Cross-references: GDB:127754; OMIM:131222	C;Genetics:		
R;An, S.; Dickens, M.A.; Bleu, T.; Hallmark, O.G.; Goetzl, E.J.	Db	68 PQLPV-----ADQVN----ITEFYN----KESLSSFKENENTQCGBNFMIDBCFMVL 111	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
Biochem. Biophys. Res. Commun. 231, 619-622, 1997	Qy	3 PTSVPLKAIRSSVSVDYVNYDILVRYHNTYTGKLNSADKENSILK-----C 47	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Title: Molecular cloning of the human Edg2 protein and its identification as a functional gene. Molecular cloning of the human Edg2 protein and its identification as a functional gene.	Db	112 NP\$QQLAIAVLISLITGFTVLENLVLYCVLHSRSURCRPSYHFIGSLSLAVADLGSVIVFV 171	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Reference number: JCS293; MUID:97224397; PMID:9070858	Qy	48 -----TSVVFILICCPFILENIPVLLTWKTFPH-RPMYYFIGNLALSLLAGVAYT 99	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
B;Contents: lung	Db	172 YSFIDPHFVHFRKDSRNVLFLKGVTASFASVGSFLPLTIAIYIS-----IRPLAYER 226	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Accession: JCS293	Qy	100 ANLLSGATTYKLTPAQWFLREGSMFVALSASVPSLALIAIERYITMMLKOKLNGSNNFR 159	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Status: nucleic acid sequence not shown	Db	227 IVTRPAAVVAFCMLMTIAIVLVLQVCSDFIPLPHIDSTYLMFWIGTTSV 286	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Residues: 1-364 <DNA>	Qy	160 LF-----LLISAC--WVISLIGGGPQMGNATISAUSSCSTVPLPYHKYILFCFTYFTLL 213	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
A;Cross-references: UNIPROT:Q96633; UNIPARC:UPI0000050403; GB:U80811; NID:91857424; PIDN:	Db	287 LLFIV--YAMMYILWKAHSHAVRMIQRTQKSIIHTSEDGKVQVTRPDQAMAIRLAKT 344	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
C;Superfamily: G protein-coupled receptor edg-1	Qy	214 LLSIVLIVCRLYSVLRTRSRLLF-----RKNTSKASRSEENVALLKT 256	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
Query Match Score: 15.0%; Best Local Similarity: 27.2%; Matches: 108; Conservativeness: 72; Niematches: 167; Indels: 50; Gaps: 10;	Db	345 LVLILVLLICWGPGLIAIMYDVGIQNLKLIKTVF--AFCGMLCLINSTNPVYALRSK 402	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
Matches: 108; Conservativeness: 72; Niematches: 167; Indels: 50; Gaps: 10;	Db	257 VIVLVSFPIACTAPLEFLILLDVGCKV-KTCIDLPRAEYPLVAVLNSGTNPIVTLTNK 315	Query Match Score: 14.6%; Best Local Similarity: 27.3%; Pred. No. 1.6e-21; Matches: 102; Conservative: 71; Mismatches: 129; Indels: 72; Gaps: 12;		
Qy	59 QERMTAGDNPQLVADPNITFYPNCFENBENIQCGENFMDIBCFMVNLNPQQQLA 118	Db	403 DLRAFRSMMPFSC 416		
Db	13 QOPTANEPQC-----FYNEIAFFPYNRSGKHATE-----WNTVSKLV 52	Db	316 EMRAFTRIMSPSCCK 329		
Qy	119 IAVLSLTLGFTVLENLVLYCVLHSRSURCRPSYHFIGSLSLAVADLGSVIFVSPIDFH 178	Qy			
Db	53 MG-LGIVTCIFMLANTLVMAIYNNRFHF-PIYTMANAAADPAGLAYFYMENGT 110	Db			
Qy	179 VPHRKDSRNVLFLKGVTASFASVGSFLPLTIAIYISHLRPLAYKRVTRPKAVAF 238	Qy			

Qy	409	-RSMEPSCGTAAQPLDNS	425	F;193-211/Domain: transmembrane #status predicted <TM5> F;240-263/Domain: transmembrane #status predicted <TM6> F;276-297/Domain: transmembrane #status predicted <TM7>
Db	324	IRIISCKCPNGDSAGKPKRBLIPGMNPSRSKSDNS	359	Query Match Score 305; DB 2; Length 325; Best Local Similarity 27.5%; Pred. No. 1.2e-17; Matches 95; Conservative 66; Mismatches 118; Indels 66; Gaps 13;
RESULT 10				
S71323	alpha-1A adrenergic receptor - Japanese medaka	C;Species: Oryzias latipes (Japanese medaka)	Qy 92 NEENIOTGENFMDFIBCFMVLNAPS---QQLIAIV-LSLTLGTFPTVLENLLVLCVIGHSRSL 147	C;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;137-63/Domain: melanocortin receptor; receptor; transmembrane protein
C;Accession: S71323	R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.	A;Keywords: G protein-coupled receptor	Db 17 SEDNT-LGQN-----VANKSSACDMGIAVEFLGLVSLNLLVIGAVIYKNKL 67	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;84-10/Domain: transmembrane #status predicted <TM1>
R;Yasuoka, A.; Abe, K.; Arai, S.; Emori, Y.	Bur. J. Biochem. 235, 501-507, 1996	A;Article: Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Medaka. Molecular cloning and functional expression of the alpha-1-A-adrenoceptor of Medaka.	Qy 148 RCRPSYHFGTGSLAYADLIGSVIFVYFSIDFHVFHRKD--SRNVLFLFKLGYY----TASF 200	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;112-138/Domain: transmembrane #status predicted <TM2>
A;Reference number: S71323; MUID:96184522; PMID:8654394	A;Accession: S71323	A;Molecule type: DNA	Db 68 H-SPPXFGTGSLAYADMLVEMSNAVETYLINNNKHVLAFTYRHDIVFDRKDNFDOMICISV 126	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;164-185/Domain: transmembrane #status predicted <TM3>
A;Residues: 1-477 <AS>	A;Note: it is uncertain whether Met-1 or Met-8 is the initiator	C;Superfamily: vertebrate rhodopsin	Qy 201 TASVSSLFLTAIARYSISHLPLAYKRVTRPKAVVAFCLMWTTIAIVAVPLGLHNCEKLV 260	C;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;186 VIVC-----LISMPTMLFFMWLFLPVAYMYILWAHSAHVRMTORGTKSIIH 320
A;Cross-references: UNIPARC:UPI00012ED53; EMBL:D63859	C;Superfamily: vertebrate rhodopsin	Db 127 VASMCSSLATAVDYRIFTYFALRYHMTARRSGVTLIACIWTCISCGVPIIYVB-SKY 185	Db 261 QSVCSDFPHIDETYLTMFWIGTVSTYLLPTVAYMYILWAHSAHVRMTORGTKSIIH 320	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270
Qy 107 CEMVNLANS-QQLIAIV-TSLTGTFT--VLENLLVCLVILHSRSLRCPSYHFGTGSLAY 162	Qy 201 TASVSSLFLTAIARYSISHLPLAYKRVTRPKAVVAFCLMWTTIAIVAVPLGLHNCEKLV 260	Db 186 VIVC-----LISMPTMLFFMWLFLPVAYMYILWAHSAHVRMTORGTKSIIH 320	Db 291 TSEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNNKLTKTVFA 380	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;381 FCIM-----LCLLNSTVNPIIYALRSKDLRAFRSMPPSCEG 417
Db 20 CSHVLAFLBNVTKAVVFLGIVGIFFILEGVIGNILVILSVCHRHQ-TVTYYPINLAVA 78	Db 291 TSEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNNKLTKTVFA 380	Db 271 ACFMSYFNNYLLILMCNSVDPPLIVALARSQEMRRTFFKEI-CCCHG 314	Db 321 TSEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNNKLTKTVFA 380	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Qy 163 D-LIGSIVFYSRDTFVHEPKDSRNTYLEKIGGY-TASTTASVGSLTEIAYRISTHR 220	Db 291 TSEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNNKLTKTVFA 380	Db 291 TSEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNNKLTKTVFA 380	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 79 DLLLSSSTVLPPSAI-PEILDRLWFGRVFCNIVAAVDVLCCTASINSLVCISVDRIGVSY 137	Db 79 DLLLSSSTVLPPSAI-PEILDRLWFGRVFCNIVAAVDVLCCTASINSLVCISVDRIGVSY 137	Db 79 DLLLSSSTVLPPSAI-PEILDRLWFGRVFCNIVAAVDVLCCTASINSLVCISVDRIGVSY 137	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Qy 221 PLAYKRIVTRPKAVVACFLMVTIAIVAVPLGLMN-CBKQLOQCS-----DIPPHI 271	Db 138 PLRYPAMTRKBRALLAVMLWLSVSIGLEKGRPAPEDETYKITEBPGVAFIAVS 197	Db 138 PLRYPAMTRKBRALLAVMLWLSVSIGLEKGRPAPEDETYKITEBPGVAFIAVS 197	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 138 PLRYPAMTRKBRALLAVMLWLSVSIGLEKGRPAPEDETYKITEBPGVAFIAVS 197	Qy 272 DETYLMFWIGTVSLLFIVIAYMYILWAHSAHVR--M1QRGTOKSIIH-----T 321	Db 198 GSPYL-----PLATILAMICRVVAAQKESRGKLEGGQTEKSDBQVILMRHGNNTV 250	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Qy 322 SEDGKVQVTRPQARMATLAKTLYLIVVLLICWGPPLAIMYDVEGRKNN 372	Db 251 SEDEALR----SRTHPAFLRLKPSREKKAATLGLIVGCFVLCWLFPLVPIGSIFPAY 306	Db 251 SEDEALR----SRTHPAFLRLKPSREKKAATLGLIVGCFVLCWLFPLVPIGSIFPAY 306	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 251 SEDEALR----SRTHPAFLRLKPSREKKAATLGLIVGCFVLCWLFPLVPIGSIFPAY 306	Qy 373 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 307 RPSDTVVKITFWLGIVNSCINPITYLGSNQEFKKAKSQL 345	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Qy 373 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 307 RPSDTVVKITFWLGIVNSCINPITYLGSNQEFKKAKSQL 345	Db 307 RPSDTVVKITFWLGIVNSCINPITYLGSNQEFKKAKSQL 345	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 307 RPSDTVVKITFWLGIVNSCINPITYLGSNQEFKKAKSQL 345	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Qy 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 452 KLIKTVAFCPSMCLANSTNPVIIYALSKDLRHAFRM 411	Db 229 -----RORASMGATIUTMLGIFIVCWSPSPFHLMISCPQN----VIC 270	A;Cross-references: UNIPARC:P35345; UNIPARC:UPI00012ED53; GB:L27081; MID:9435606; PIDN: F;314 RESULT 12
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F:232-257/Domain: transmembrane #status predicted <TM5>	Db	118 ASVYPSLLAIAIERQVAI--AKVKLYGSDSCKRMLIGASWLILGGHPILGNCL 173
P:287-310/Domain: transmembrane #status predicted <TM6>		
P:324-344/Domain: transmembrane #status predicted <TM7>		
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Qy 115 QQLAIAY-LSLTIGFTVYLENLVCLHRSRLRCRSPYHFGSLAVADLIGSVFVYVS 173	Qy	318 IHTSEDGKVQVTRPDAARMAIRAKPLVLVLLVLLCIGPILALAMYD-----VF 368
Db 81 EENGIAVEVFLTGVLGSLENLVLIGAVTKNKLH-SMPYFYGSLLAVADMVMSNAWE 139	Db	222 -----DYAGP----QTLALAKTVTIVLGVFTICWLPAFSLILIDSTCPVRACBVIL 267
Qy 174 FIDFHVFHRKD--SRNFVFLFKLGSGV---TASFTASYGSLFITAIARYISITHRPLAYKR 226	Qy	369 GRNNKLKTVFAPCSMCLLNSTVNPIYAIRSKDR 405
Db 140 TVTYLNNKKHLVTAATPVFRHIDVFDMSMCISVVASNCSSLLAIAVDRYITFYALRYHH 199	Db	268 YKAHYF---FAFAT---LNSLNPVITYWRSRDLR 296
Qy 227 IVTRPKAVVAFACLMWTTIAVIAVPLGLWCNCBKLQSYCSDFPHDETYLMFWIGTVS 286		RESULT 14
Db 200 IMPARRSIVTIACTIWTCISCGIVFVIIYE-SKXVIIIC-----LISMFTM 244		S40454
Qy 287 LLFIVYAMYILWKAHSHAVRMQRTGKSIITHSENGKVQVTRPDAARMIRAKLTKLV 346		G protein-coupled receptor GPCR21 - mouse
Db 245 LFFMVSLTHMPMLARNVKVRITAASPRNTNSVRQTSRNGAI-----TLT 288		C;Species: Mus musculus (house mouse)
Qy 347 LILVVLLICWGPLLAIMYDVFGRMKNDIJKTFCAFCSM---LCLLNSTVNPIYAIRSKD 403		C;Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Db 289 MLGLIFIVCWSPPTFLHLLMISCPQNYYCSCFCMSYFNMYLILMCNSVIDPLIYALRSQE 348		C;Accession: S40454
Qy 404 LRHAFRSMPPSCSEGTAQP 421		A;Title: Molecular cloning of a novel putative G protein-coupled receptor (GPCR21) which A;Reference number: MUID:94085630; PMID:8262253
Db 349 MRRTEFKEIV-CCHGFRP 365		A;Accession: S40454
		A;Status: Preliminary
		A;Molecule type: mRNA
		A;Residues: 1-330 <SAE>
		A;Cross references: UNIPROT:P35413; UNIPARC:UPI0000025C17; GB:D21062; NID:9155487; PIDN
		C;Superfamily: melanocortin receptor
		C;Keywords: G protein-coupled receptor; phosphoprotein; transmembrane protein
RESULT 13		
JC1465		
probable G protein-coupled receptor - rat		Query Match Score 12.2%; Score 295.5; DB 2; Length 330;
C;Species: Rattus norvegicus (Norway rat)		Best Local Similarity 28.0%; Pred. No. 7.8e-17;
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004		Matches 90; Conservative 61; Mismatches 125; Indels 45; Gaps 13;
Db 111 LNPQQQLAAIVNTSLTGTETVLENLVLCVILHSURCRPSYHFIGSLAVADLGLSVIF 170		Query Match Score 12.2%; Score 295.5; DB 2; Length 330;
Db 36 LLPSRPAWDVLLCS-GTLVSCRNALVAVIATGPATRA-PMFSLVSLAVADLLAGIQL 93		Best Local Similarity 28.0%; Pred. No. 7.8e-17;
Qy 171 VTSF-IDPFVFRKDSANVFLPKLGVTASFTASVGSFLLTIAIRYSIHLRPLAKRVT 229		Matches 90; Conservative 61; Mismatches 125; Indels 45; Gaps 13;
Db 94 VLHFAADECII---GSPEMSLMLVGVLAMAFAASIGSLATVDRYLSLYNALTYYSETT 149		Query Match Score 12.2%; Score 295.5; DB 2; Length 330;
Qy 230 RPKAVVACFLMPTIAVIAVPLGLGCNEKLOSVCSDIFPHDETYLMFWIGTVS 289		Best Local Similarity 28.0%; Pred. No. 7.8e-17;
Db 150 VTRYVMLAVNGALGGLGVPLAWNRCDGLTGTVVYP-LSKRNL---VVLNATAFF 203		Matches 90; Conservative 61; Mismatches 125; Indels 45; Gaps 13;
Qy 290 IVYAMYILWKAHSHAVRMQRTGKSI-SIIHTSEDGKVQVTRPDAARMIRAKLTKLV 348		Query Match Score 12.2%; Score 295.5; DB 2; Length 330;
Db 204 MVFG---IMLOLYAQICRIVRAQOALQRHLPASHYVATRKIGIA-----TLRVV 252		Best Local Similarity 28.0%; Pred. No. 7.8e-17;
Qy 349 LVVDTLICWGPLLAIMYDVFGRMKNDIJKTFCAFCSM-CLLNSTVNPIYAIRSKDHLR 407		Matches 90; Conservative 61; Mismatches 125; Indels 45; Gaps 13;
Db 253 LGAAACW---LPFTVYCLLGADS-S-PRLYTYLTLPATYNMSMNPVYIAFPNQDVQKV 307		Query Match Score 12.2%; Score 295.5; DB 2; Length 330;
Qy 408 -----FRSMFPS 414		Best Local Similarity 29.4%; Pred. No. 6.9e-17; Length 352;
Db 308 LWIACCCTSSTSFRSRSPS 328		Matches 99; Conservative 48; Mismatches 117; Indels 73; Gaps 12;
RESULT 15		
Qy 92 NEENIQGENFMFDIECFMVLNPQSQLAVIAVSLTLGTETVLENLVLCHRSRSLRCP 151		
Db 10 NPXQVQEHNNTKETLDMQTPSRKVAASF-IILCCAVVENLVLAVARNSKFH 67		I16416 melanocyte-stimulating hormone receptor - sheep
Qy 152 SYHFQGSLLAVADLIGSVIY-----YSFIDEHYFHRKDSRNVYFLKGQVTAFT 201		C;Species: Ovis orientalis aries, Ovis aries (domestic sheep)
Db 68 MYLFTGNLNLASDLLAGVAVANTULSGPYTLSPLQWFARE-----GSAFTLS 117		C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 09-Jul-2004
		R;Barrett, P.; MacDonald, A.; Helliwell, R.; Davidson, G.; Morgan, P.
		J. Mol. Endocrinol. 12, 203-213, 1994

A;Title: Cloning and expression of a new member of the melanocyte- β -stimulating hormone receptor
A;Reference number: I46416; MUID:94336523; PMID:8060485
A;Accession: I46416
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residue: 1-325 <BAR>
A;Cross-references: UNIPROT:P41983; UNIPARC:UPI000012ED54; EMBL:Z31369; NID:9467692; PID
A;Note: submitted to the EMBL Data Library, March 1994
C;Superfamily: melanocortin receptor

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Qy	112	NPSQQLAINV-LSITLGTTPEVLENIYLCTILHRSRSLRCPSTYHFIGSLAVADLILGSY-	168	
Db	31	SPCEDMGIAVEFLALGTLISLLNTLVIGAIVRNRLHI-PMTPEVGSLAVADMLVLSN	89	
Qy	169	---IFVYSPIDFHVPHRKS--- RNVFLFKLGGTVASFTASWGSLLPITALARYIISTHR	220	
Db	90	FWEETTIVYLITNKVHWWADSVRLHDNP--DSMICISVVASICCSLILAIADVYTFC	146	
Qy	221	PLAYKRVV--RPKAVV--AFCLIMWTTIAIVIAVPLLGWNCEKLQSVCSDIF-PHIDB	273	
Db	147	RLRYQRIMTRGRSGAIAGIWAFC-----TSCGTIVIVYES	183	
Qy	274	TYL----MFWIGTSVLLIRIYAYMYLWKAHSAYRMIOGRTOKSLLIHTSBDGKV	327	
Db	184	TYVVVCLIAMF--LTMLLIMASLYTHMFLARTH--YRRI----AAALPGHSSV----	228	
Qy	328	QVTRDDQARNMAILRALKTLLVLLVLLICNGPILLAIMYDVGKRNKLKITVPARCS	383	
Db	229	-----RQRTGKVKGATILAMUIGFPIICMAPPEFHLMNISCPQN-----LYCSCMS	275	
Qy	384	-----MLCLLNSTNPITYALRSKDLRHAFRSM-----FPS	414	
Db	276	HENMYLILMGSVIDPLIYAFSOEMRKTFKEIVCFQGFRTPCRPPS	323	

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Job time : 42 secs

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